

Result No.	Score	Query %			DB	ID	Description
		Match	Length	Length			
1	800	100.0	154	4	AAy72840	Mouse Sta	
2	800	100.0	770	2	Aar72082	Mouse Sta	
3	800	100.0	770	2	AAW03176	Mouse Sta	
4	800	100.0	770	3	AAB12377	N-termina	
5	800	100.0	770	5	AAE14652	Murine ST	
6	800	100.0	770	6	ABU10476	Mouse STA	
7	792	99.0	720	5	AAE22055	Human STA	
8	792	99.0	769	5	ABBS7164	Mouse lsc	
9	792	99.0	769	5	AAE22054	Human STA	
10	792	99.0	769	5	AAE22056	Human pro	
11	792	99.0	770	2	AAE82995	Mouse liv	
12	792	99.0	770	2	AAE82993	Human pla	
13	792	99.0	770	2	AAE03768	Human STA	
14	792	99.0	770	4	AAE19964	Human sig	
15	792	99.0	770	5	ABG69497	Human bai	
16	792	99.0	770	5	AAE15174	Human Sta	
17	792	99.0	770	7	ADD44738	Rat Prote	
18	792	99.0	770	7	ADD44740	Human Pro	
19	792	99.0	770	8	ADN04365	Antipsori	
20	792	99.0	770	8	ADP54789	Human PRO	
21	792	99.0	793	3	AAE58442	Lung canc	
22	380	47.5	154	4	AAy72843	Mouse Sta	
23	380	47.5	680	6	ABR59713	Human sig	
24	380	47.5	701	2	AAE41335	84 kD ISG	
25	380	47.5	701	6	ABU04741	Human exp	

CC transformation: These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain; linker domain, SH2 domain and transactivation domain
XX Sequence 154 AA;
SQ Query Match 100.0%; Score 800; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.1e-77;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOWNLOQLDTRYLKQHLQYSDTFPMEIARQFLAPWIESQDWAYAASKESHATLVFHNL 60
DB 1 MAOWNLOQLDTRYLKQHLQYSDTFPMEIARQFLAPWIESQDWAYAASKESHATLVFHNL 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLIQATA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLIQATA 120
QY 121 TAAQGGQGANHTAAVVTKEQKQMLEQHLQDVRKR 154
DB 121 TAAQGGQGANHTAAVVTKEQKQMLEQHLQDVRKR 154

RESULT 2
AAR72082
ID AAR72082 standard; protein; 770 AA.
XX
AC AAR72082;
XX
DT 25-MAR-2003 (revised)
DT 27-SEP-1995 (first entry)
XX
DE Mouse Stat3 (19sf6).
XX
KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
KW receptor recognition factor; transcription factor; cellular debilitation;
KW derangement; dysfunction; interferon-gamma.
XX
OS Mus sp.
XX WO9508629-A1.
XX
XX 30-MAR-1995.
XX
XX 26-SEP-1994; 94WO-US010849.
XX
XX 24-SEP-1993; 93US-00126588.
XX 24-SEP-1993; 93US-00126595.
XX 11-MAR-1994; 94US-00212184.
XX 11-MAR-1994; 94US-00212185.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
XX WPI: 1995-139598/18.
XX N-PSDB; AAQ89340.
XX
XX Receptor recognition factor implicated in transcriptional stimulation of
PT genes - useful in drug screening assays and/or for treating cellular
PT debilitations, derangements and/or dysfunctions, etc.
XX
XX Claim 1; Page 107-110; 160pp; English.
XX
XX A fragment encoding the human Stat91 protein was used to screen a murine
CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
CC mouse gene as probe, 2 additional members of the 113-91 family of
CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
CC and 40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed
CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-

CC 2003 to correct PN field.)
XX Sequence 770 AA;
SQ Query Match 100.0%; Score 800; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 9e-77;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOWNLOQLDTRYLKQHLQYSDTFPMEIARQFLAPWIESQDWAYAASKESHATLVFHNL 60
DB 1 MAOWNLOQLDTRYLKQHLQYSDTFPMEIARQFLAPWIESQDWAYAASKESHATLVFHNL 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLIQATA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLIQATA 120
QY 121 TAAQGGQGANHTAAVVTKEQKQMLEQHLQDVRKR 154
DB 121 TAAQGGQGANHTAAVVTKEQKQMLEQHLQDVRKR 154

RESULT 3
AAW03176
ID AAW03176 standard; protein; 770 AA.
XX
AC AAW03176;
XX
DT 24-OCT-1996 (first entry)
XX
DE Mouse STAT4.
XX
KW STAT; STAT4; signal transducer and activator of transcription;
KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
KW autoimmune disease; antagonist; therapy.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Domain 398..508
FT /label= DNA binding domain
FT /note= "Claim 3, page 110"
XX
XX WO9620954-A2.
XX
XX 11-JUL-1996.
XX
XX 28-DEC-1995; 95WO-US017025.
XX
XX 06-JAN-1995; 95US-00369796.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Darnell JE, Wen Z, Horvath CM, Zhong Z;
XX WPI: 1996-333941/33.
XX N-PSDB; AAT31280.
XX
XX New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,
PT preventing or treating cellular dysfunction, e.g. oncogenesis,
PT inflammation, parasitic disease or autoimmunity.
XX
XX Disclosure; Page 87-90; 138pp; English.
XX
XX Mouse signal transducer and activator of transcription (STAT) protein
CC STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from
CC ligand-activated receptor kinase complexes followed by nuclear
CC translocation and DNA binding to activate transcription. Recombinant
CC STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from
CC splenic/thymic cells. STAT4 includes a DNA-binding domain (see also
CC AAW03167) capable of both receptor recognition and message delivery via
CC DNA binding in a receptor-ligand specific manner. STAT proteins and their
CC DNA binding domains (see also AAW03165-75) are useful for screening
CC antagonists used to inhibit STAT-mediated signal transduction and

```
CC activation of transcription
XX
SQ Sequence 770 AA;

Query Match      100.0%; Score 800; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 9e-77;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPPELQFLAPWIESQDWAYAAASKESHATLVFHNL 60
   |||||
DB 1 MAQWNQLQQLDTRYLKQLHQLYSDFPPELQFLAPWIESQDWAYAAASKESHATLVFHNL 60
   |||||

OY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOATA 120
   |||||
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOATA 120
   |||||

OY 121 TAAQGGQANHPHTAAVTEKQMLEQHLQDVRRK 154
   |||||
DB 121 TAAQGGQANHPHTAAVTEKQMLEQHLQDVRRK 154
   |||||

RESULT 4
AAB12377
ID AAB12377 standard; peptide; 770 AA.
XX
AC AAB12377;
XX
DT 08-NOV-2000 (first entry)
XX
DE N-terminal domain of murine STAT-3 protein.
XX
KW STAT; signal transducer and activator of transcription; crystal;
KW drug design; murine.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Region 4..9 /label= Alpha helix 1
FT Region 12..21 /label= Alpha helix 2
FT Region 19..21 /label= 3(10) helix of alpha helix 2
FT Region 28..33 /label= Alpha helix 3
FT Region 35..40 /label= Alpha helix 4
FT Region 43..47 /label= Alpha helix 5
FT Region 50..73 /label= Alpha helix 6
FT Region 77..96 /label= Alpha helix 7
FT Region 99..119 /label= Alpha helix 8
XX
XX US6087478-A.
XX
XX 11-JUL-2000.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX
XX WPI; 2000-505108/45.
XX
XX New crystals of an N-terminal fragment of a signal transducer and
XX activator of transcription that effectively diffracts x-rays, useful for
XX drug screening and development.
XX

XX Disclosure; Fig 1; 42pp; English.
XX
CC The present invention relates to a crystal of an N-terminal fragment of a
CC signal transducer and activator of transcription (STAT) protein. The
CC crystal effectively diffracts x-rays, allowing the determination of the
CC atomic coordinates of the N-terminal domain to a resolution of greater
CC than 5.0 Angstroms. The present sequence is the N-terminal domain of the
CC murine STAT 3 protein. The N-terminal domain enables STAT dimers to
CC interact and bind DNA cooperatively, a mechanism important for gene
CC activation. The crystals are useful in drug screening and development by
CC selecting a potential drug by performing rational drug design with the 3-
CC dimensional structure determined for the crystal
XX
SQ Sequence 770 AA;

Query Match      100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 9e-77;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPPELQFLAPWIESQDWAYAAASKESHATLVFHNL 60
   |||||
DB 1 MAQWNQLQQLDTRYLKQLHQLYSDFPPELQFLAPWIESQDWAYAAASKESHATLVFHNL 60
   |||||

OY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOATA 120
   |||||
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLLOATA 120
   |||||

OY 121 TAAQGGQANHPHTAAVTEKQMLEQHLQDVRRK 154
   |||||
DB 121 TAAQGGQANHPHTAAVTEKQMLEQHLQDVRRK 154
   |||||

RESULT 5
AAB14652
ID AAB14652 standard; protein; 770 AA.
XX
AC AAB14652;
XX
DT 16-JUL-2002 (first entry)
XX
DE Murine STAT3 protein.
XX
KW Signal transducer and activator of transcription; STAT3;
KW drug development; drug discovery; crystal; inflammation; allergy; asthma;
KW leukaemia; anaemia; neutropenia; thrombocytopaenia; cancer; obesity;
KW viral disease; growth retardation; murine.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Domain 1..130 /note= "Conserved N-terminal domain of the STAT family"
FT FT
XX
XX US6312887-B1.
XX
XX 06-NOV-2001.
XX
XX 24-APR-2000; 2000US-00556273.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX
XX WPI; 2002-033337/04.
XX
XX Identifying compounds that bind to signal transducer and activator of
XX transcription proteins, useful for the production of new drugs.
XX
XX Example; Col 47-50; 44pp; English.
XX
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CC The invention relates to methods for detecting compounds that bind to
 CC signal transducer and activator of transcription (STAT) proteins for the
 CC discovery and development of new drug compounds based on the structural
 CC properties of the protein crystal. The methods include: identifying a
 CC compound that binds to the N-terminal domain of a STAT protein,
 CC identifying a compound that enhances or diminishes the binding of the
 CC dimeric STAT proteins to each other and/or their nucleic acid binding
 CC site; or identifying a compound that enhances or diminishes the ability
 CC of STAT protein dimers to induce the expression of a gene operably under
 CC the control of a promoter containing at least two adjacent weak binding
 CC sites for STAT protein dimers. The methods are used for identifying new
 CC drugs. An antagonist of STAT N-terminal dimeric interactions that
 CC inhibits the binding of the STAT dimers to adjacent weak binding sites on
 CC a promoter of a gene, could be useful as drugs in the treatment of
 CC diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other
 CC hand, an agonist of N-terminal dimeric interactions between STAT dimers,
 CC can be used as drugs in the treatment of diseases e.g. anaemia,
 CC neutropaenia, thrombocytopaenia, cancer, obesity, viral diseases and
 CC growth retardation. The present sequence is murine STAT3 protein
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 800; DB 5; Length 770;
 Best Local Similarity 100.0%; Pred. No. 9e-77; Indels 0; Gaps 0;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
 DB 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
 QY 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMIARIVARCLWEESRLLOQTAA 120
 DB 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMIARIVARCLWEESRLLOQTAA 120
 QY 121 TAAQGGQGANHPHTAAVVTKEQQLMEOHLOQDVRRK 154
 DB 121 TAAQGGQGANHPHTAAVVTKEQQLMEOHLOQDVRRK 154

RESULT 6
 ABU10476
 ID ABU10476 standard; protein; 770 AA.
 XX
 AC ABU10476;
 DT 06-AUG-2003 (first entry)
 XX
 DE Mouse STAT3 protein..
 XX
 KW Mouse; signal transducer and activator of transcription; drug design;
 KW drug screening; STAT-STAT dimer interaction; STAT3.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 4..9 /label= alpha_helix_1
 FT Region 12..21 /label= alpha_helix_2
 FT /note= "Residues 19-21 form a 3 helix"
 FT Region 28..33 /label= alpha_helix_3
 FT Region 35..40 /label= alpha_helix_4
 FT Region 43..47 /label= alpha_helix_5
 FT Region 50..73 /label= alpha_helix_6
 FT /note= "Residues 57, 61, 64, 68 and 71 contribute to
 FT packing of the coiled-coil"
 FT Region 77..96 /label= alpha_helix_7
 FT /note= "Residues 79, 83, 86, 90 and 94 contribute to

FT Region packing of the coiled-coil"
 FT 99..119 /label= alpha_helix_8
 XX
 PN US2003003563-A1.
 XX
 PD 02-JAN-2003.
 XX
 XX 19-OCT-2001; 2001US-00045792.
 XX
 PR 23-JAN-1998; 98US-00012710.
 PR 24-APR-2000; 2000US-0056273.
 XX
 PA (VINK/) VINKEMEIER U.
 PA (MOAR/) MOAREFI I.
 PA (DARN/) DARNELL J E.
 PA (KURI/) KURIYAN J.
 XX
 PI Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
 XX
 DR WPI; 2003-447354/42.
 XX
 PT New crystal having an N-terminal domain of a STAT protein performing X-
 PT ray crystallographic studies, useful for screening drugs that enhance or
 PT inhibit STAT-STAT dimer interactions.
 XX
 PS Disclosure; Page 25-26; 46pp; English.
 XX
 CC The invention relates to a crystal of an N-terminal domain of signal
 CC transducer and activator of transcription (STAT) protein, where the
 CC crystal effectively diffracts X-rays for the determination of the atomic
 CC coordinates of the N-terminal domain of the STAT protein to a resolution
 CC of greater than 5.0 Angstrom. The methods and compositions are useful for
 CC the design and screening of drugs that enhance or inhibit STAT-STAT dimer
 CC interactions. The present sequence represents the amino acid sequence of
 CC mouse STAT3 protein
 XX
 SQ Sequence 770 AA;
 Query Match 100.0%; Score 800; DB 6; Length 770;
 Best Local Similarity 100.0%; Pred. No. 9e-77; Indels 0; Gaps 0;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
 DB 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVFHNL 60
 QY 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMIARIVARCLWEESRLLOQTAA 120
 DB 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMIARIVARCLWEESRLLOQTAA 120
 QY 121 TAAQGGQGANHPHTAAVVTKEQQLMEOHLOQDVRRK 154
 DB 121 TAAQGGQGANHPHTAAVVTKEQQLMEOHLOQDVRRK 154
 RESULT 7
 AAEE22055
 ID AAEE22055 standard; protein; 720 AA.
 XX
 AC AAEE22055;
 XX
 DT 25-JUL-2002 (first entry)
 XX
 DE Human Stat3beta protein.
 XX
 KW Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;

KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion; Statbeta.
 XX Homo sapiens.
 OS
 PH Key Location/Qualifiers
 FT Misc-difference 713..714
 FT /note="Encoded by ACA CCA TTC"
 XX
 PN WO200220032-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028254.
 XX
 PR 08-SEP-2000; 2000US-0231212P.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 PI Yu H, Pardoll D, Jove R, Dalton W;
 XX
 DR WPI: 2002-362218/39.
 DR N-PSDB; AAD35066.
 XX
 XX Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.
 XX
 PS Disclosure; Page 87-89; 94pp; English.
 XX
 CC The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g. bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC Stat3beta protein
 XX
 SQ Sequence 720 AA;
 Query Match 99.0%; Score 792; DB 5; Length 720;
 Best Local Similarity 98.7%; Pred. No. 6e-76;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNLQQLDTRYLKHQLHLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
 DB 1 MAQWNLQQLDTRYLKHQLHLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFPHNL 60

QY 61 LGEIDQOYSRFLQESNVLYOHNLRRRIKQFLQSYLKEPKMEIARIVARCLWEESRLLOTAA 120
 DB 61 LGEIDQOYSRFLQESNVLYOHNLRRRIKQFLQSYLKEPKMEIARIVARCLWEESRLLOTAA 120
 QY 121 TAAQGGQGANHPTAAVVTKEQKQMLEQHLQDVRKR 154
 DB 121 TAAQGGQGANHPTAAVVTKEQKQMLEQHLQDVRKR 154
 RESULT 8
 ABB57164
 ID ABB57164 standard; protein; 769 AA.
 XX
 AC ABB57164;
 XX
 DT 07-MAR-2002 (first entry)
 XX
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:398.
 XX
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
 XX
 OS Mus musculus.
 XX
 PN WO200188188-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-JP004192.
 XX
 PR 18-MAY-2000; 2000JP-00145977.
 XX
 PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX
 DR WPI: 2002-034733/04.
 DR N-PSDB; ABI199454.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX
 PS Claim 2; Page 1084-1087; 2690pp; English.
 XX
 CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI199202 to ABI19912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI19913 and ABI199914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX
 SQ Sequence 769 AA;
 Query Match 99.0%; Score 792; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 6.5e-76;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNLQQLDTRYLKHQLHLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
 DB 1 MAQWNLQQLDTRYLKHQLHLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
 QY 61 LGEIDQOYSRFLQESNVLYOHNLRRRIKQFLQSYLKEPKMEIARIVARCLWEESRLLOTAA 120

Db 61 LGIEDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETIARIVARCLWEESRLQTAA 120
 QY 121 TAAQGGQGANHTAAVTEKQOMLEQHLQDVRRK 154
 Db 121 TAAQGGQGANHTAAVTEKQOMLEQHLQDVRRK 154

RESULT 9
 AAE22054
 ID AAE22054 standard; protein; 769 AA.

XX AC AAE22054;
 XX DT 25-JUL-2002 (first entry)
 XX DE Human Stat3 protein.

XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.

XX Homo sapiens.
 XX WO200220032-A1.
 XX 14-MAR-2002.
 XX 10-SEP-2001; 2001WO-US028254.
 XX 08-SEP-2000; 2000US-0231212P.

XX (UYJO) UNIV JOHNS HOPKINS.
 XX (UYSP-) UNIV SOUTH FLORIDA.
 XX Yu H, Pardoll D, Jove R, Dalton W;
 XX WPI: 2002-362218/39.
 XX N-PSDB; AAD35065.
 XX Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.

XX Disclosure; Page 83-85; 94pp; English.
 XX The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,

CC Gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human Stat3
 CC protein
 XX
 SQ Sequence 769 AA;

Query Match 99.0%; Score 792; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 6.5e-76;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNQLQLDTRYLQKHLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
 Db 1 MAQWNQLQLDTRYLQKHLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
 QY 61 LGIEDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETIARIVARCLWEESRLQTAA 120
 Db 61 LGIEDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETIARIVARCLWEESRLQTAA 120
 QY 121 TAAQGGQGANHTAAVTEKQOMLEQHLQDVRRK 154
 Db 121 TAAQGGQGANHTAAVTEKQOMLEQHLQDVRRK 154

RESULT 10
 ID AAE22056
 XX AAE22056 standard; protein; 769 AA.

XX AAE22056;
 XX 25-JUL-2002 (first entry)
 XX Human protein related to angiogenesis regulation.

XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.

XX Homo sapiens.
 XX WO200220032-A1.
 XX 14-MAR-2002.
 XX 10-SEP-2001; 2001WO-US028254.
 XX 08-SEP-2000; 2000US-0231212P.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX (UYSP-) UNIV SOUTH FLORIDA.

XX Yu H, Pardoll D, Jove R, Dalton W;
 XX WPI: 2002-362218/39.
 XX Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a

PT compound that modulates the activity of a signal transducer and activator
 of transcription 3.

XX Disclosure; Page 83-85; 94pp; English.

XX The invention relates to a method of modulating angiogenesis and immune
 response. Method involves administering to an individual a compound that
 modulate the activity of signal transducer and activator of transcription
 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 hypoxic or ischaemic condition or disorder which is the result of stroke,
 ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 tissue ischaemia in the lower extremities, infarction, trauma, vascular
 occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC protein related to angiogenesis regulation

XX SQ Sequence 769 AA;

Query Match 99.08; Score 792; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 6.5e-76;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
 DB 1 MAQWNLQQLDTRYLEQLHQLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
 QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTAA 120
 DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTAA 120
 QY 121 TAAQGGQGANHTAAVTEKQMLQHLQDVRRK 154
 DB 121 TAAQGGQGANHTAAVTEKQMLQHLQDVRRK 154

RESULT 11

AAR82995
 ID AAR82995 standard; protein; 770 AA.

XX AAR82995;

XX 25-MAR-1996 (first entry)

XX Mouse liver acute phase response factor.

XX Mouse; acute phase response factor; transcription factor; interleukin-6;
 KW signal transduction; liver; antibody; antisense; ribozyme;
 KW antiinflammatory; antitumor; hypotensive; therapy.

XX Mus musculus.

XX EP676469-A2.

XX 11-OCT-1995.

XX

PF 29-MAR-1995; 95EP-00104670.
 XX 04-APR-1994; 94JP-00065825.
 XX (KISH/) KISHIMOTO T.

XX Akira S, Kishimoto T;

XX WPI; 1995-346089/45.

DR N-PSDB; AAT05619.

XX New acute phase response factor - for developing inhibitory agents for
 treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
 diseases.

XX Claim 10; Page 20-22; 31pp; English.

XX The sequence represents a mouse acute phase response factor (APRF), a
 transcription factor related to signal transmission of interleukin-6 (IL-
 6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
 library using a polymerase chain reaction product (amplified using
 primers derived from an IL-6-treated mouse liver peptide) as a probe.
 CC APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
 CC ribozymes, may be used to treat diseases induced by IL-6, e.g.
 CC inflammatory disease, leukemia, cancer, osteoclastia, pulmonary
 CC hypertension, etc

XX SQ Sequence 770 AA;

Query Match 99.0%; Score 792; DB 2; Length 770;
 Best Local Similarity 98.7%; Pred. No. 6.5e-76;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
 DB 1 MAQWNLQQLDTRYLEQLHQLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
 QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTAA 120
 DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTAA 120
 QY 121 TAAQGGQGANHTAAVTEKQMLQHLQDVRRK 154
 DB 121 TAAQGGQGANHTAAVTEKQMLQHLQDVRRK 154

RESULT 12

AAR82993
 ID AAR82993 standard; protein; 770 AA.

XX AAR82993;

XX 25-MAR-1996 (first entry)

XX Human placenta acute phase response factor protein.

XX human; acute phase response factor; transcription factor; interleukin-6;
 KW signal transduction; placenta; antibody; antisense; ribozyme;
 KW antiinflammatory; antitumor; hypotensive; therapy.

XX Homo sapiens.

XX EP676469-A2.

XX 11-OCT-1995.

XX 29-MAR-1995; 95EP-00104670.

XX 04-APR-1994; 94JP-00065825.

XX (KISH/) KISHIMOTO T.

XX Akira S, Kishimoto T;

XX WPI; 1995-346089/45.
DR N-PSDB; AAT05616.
XX
PT New acute phase response factor - for developing inhibitory agents for
PT treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
PT diseases.
XX
PS Claim 3; Page 9-12; 31pp; English.
XX
CC The sequence corresponds to a human acute phase response factor (APRF), a
CC transcription factor related to signal transmission of interleukin-6 (IL-
CC 6). The protein is expressed from a human placenta cDNA, isolated using
CC an IL-6-treated mouse liver cDNA probe. APRF-inhibitors, e.g. antibodies,
CC antisense oligonucleotides or ribozymes, may be used to treat diseases
CC induced by IL-6, e.g. inflammatory disease, leukemia, cancer,
CC osteoclasia, pulmonary hypertension, etc
XX
SQ Sequence 770 AA;
Query Match 99.0%; Score 792; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 6.5e-76;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMEQLRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMEQLRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Qy 61 LGEIDQOYSRFLQESNVLYQHNLRRIKOFLQSRYLEKPMELIARIVARCLWEESRLQOTAA 120
Db 61 LGEIDQOYSRFLQESNVLYQHNLRRIKOFLQSRYLEKPMELIARIVARCLWEESRLQOTAA 120
Qy 121 TAAQGGQGANHTAAVVTKEQQLMQLQHLQDVRRK 154
Db 121 TAAQGGQGANHTAAVVTKEQQLMQLQHLQDVRRK 154
RESULT 13
AAY03768
ID AAY03768 standard; protein; 770 AA.
XX
AC AAY03768;
XX
DT 11-JUN-1999 (first entry)
XX
DE Human STAT3 allelic variant.
XX
KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;
KW intracellular transcription factor; interleukin-6; medicament; variant;
KW pharmaceutical; autoimmune disease; inflammatory; human.
XX
OS Homo sapiens.
XX
PN EP905234-A2.
XX
PD 31-MAR-1999.
XX
PF 18-FEB-1998; 98EP-00102774.
XX
PR 16-SEP-1997; 97EP-00116061.
XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Serlupi-Crescenzi O, Della Pietra L;
XX
DR WPI; 1999-192664/17.
DR N-PSDB; AAX29281.
XX
PT New human Signal Transducer and Activator of Transcription 3 (STAT3)
PT allelic variant useful for treatment of autoimmune and inflammatory
PT disease.
XX
PS Claim 2; Page 9-13; 32pp; English.

XX The present sequence represents a predominant allelic variant of human
CC Signal Transducer and Activator of Transcription 3 (STAT3) protein, an
CC intracellular transcription factor which mediates IL-6 signals. The
CC encoding sequence differs from the original published human STAT3 gene
CC sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3
CC DNA molecule can be used for the recombinant expression of the variant.
CC STAT3 protein is useful as a medicament or pharmaceutical composition for
CC treatment of autoimmune or inflammatory diseases
XX
SQ Sequence 770 AA;
Query Match 99.0%; Score 792; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 6.5e-76;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMEQLRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMEQLRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Qy 61 LGEIDQOYSRFLQESNVLYQHNLRRIKOFLQSRYLEKPMELIARIVARCLWEESRLQOTAA 120
Db 61 LGEIDQOYSRFLQESNVLYQHNLRRIKOFLQSRYLEKPMELIARIVARCLWEESRLQOTAA 120
Qy 121 TAAQGGQGANHTAAVVTKEQQLMQLQHLQDVRRK 154
Db 121 TAAQGGQGANHTAAVVTKEQQLMQLQHLQDVRRK 154
RESULT 14
AAB19964
ID AAB19964 standard; protein; 770 AA.
XX
AC AAB19964;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human signal transducer and activator of transcription STAT-3.
XX
KW STAT-3; signal transducer and activator of transcription 3; human;
KW crystal; drug screening.
XX
OS Homo sapiens.
XX
FH Location/Qualifiers
FT Domain 134..320
FT /note= "coiled-coil domain"
FT Domain 321..493
FT /note= "DNA-binding domain"
FT Domain 494..583
FT /note= "linker domain"
FT Domain 584..688
FT /note= "SH2 domain"
FT Region 689..717
FT /note= "C-terminal tail segment"
FT Modified-site 705
FT /note= "O-phosphorylated"
XX
PN US6160092-A.
XX
PD 12-DEC-2000.
XX
PF 29-MAY-1998; 98US-00087465.
XX
PR 29-MAY-1998; 98US-00087465.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Chen X, Darnell JE, Kuriyan J, Vinkemeier U, Zhao Y, Jeruzalmi D;
PI WPI; 2001-101568/11.
DR N-PSDB; AAB89229.
XX

PT Novel crystal useful in drug screening assays, comprises portion of
PT signal transducer, activator of transcription and duplex DNA.

XX Disclosure; Col 67-71; 206pp; English.

PS The present sequence is that of human signal transducer and activator of
XX transcription 3 (STAT-3). The invention provides a crystal of a core
CC portion of a STAT protein in dimer form with an 18-mer duplex DNA (see
CC AAA89233) that contains a binding site for the STAT dimer. The core
CC portion comprises a coiled-coil domain comprising 4 long helices, a DNA
CC binding domain which contains an immunoglobulin-like fold, a C-terminal
CC SH2 domain and a domain that links the DNA binding and SH2 domains. The
CC crystal is of sufficient quality to perform X-ray crystallography
CC studies. Methods of preparing the crystals are included in the invention.
CC Knowledge of the STAT protein's 3-dimensional structure will aid in
CC structure-based drug design. The crystal can be used in drug screening
CC assays to identify agonist and antagonist compounds. Antagonists can be
CC used to treat inflammation, allergy, asthma and leukaemia, and agonists
CC to treat anaemia, neutropenia, thrombocytopenia, cancer, obesity, viral
CC diseases, growth retardation, and other conditions characterized by
CC insufficient STAT activity

XX Sequence 770 AA;

Query Match 99.0%; Score 792; DB 4; Length 770;

Best Local Similarity 98.7%; Pred. No. 6.5e-76;

Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQHLQHSYDTPFMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60

DB 1 MAQWNLQQLDTRYLKQHLQHSYDTPFMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60

QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMPIARIVARCLWEESRLQTA 120

DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMPIARIVARCLWEESRLQTA 120

QY 121 TAAQGGQGANHPPTAAVVTKEQQLQHLQDVRRK 154

DB 121 TAAQGGQGANHPPTAAVVTKEQQLQHLQDVRRK 154

RESULT 15

ABG69497

ID ABG69497 standard; protein; 770 AA.

XX AC ABG69497;

DT 21-OCT-2002 (first entry)

XX Human bait protein STAT3.

XX Human; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;

KW non-insulin diabetes mellitus; obesity; selected interacting domain; SID;

KW protein-protein interaction map; PWM; anorectic; metabolic disorder.

XX Homo sapiens.

XX WO200253726-A2.

XX 11-JUL-2002.

XX 28-DEC-2001; 2001WO-EP015423.

XX 02-JAN-2001; 2001US-0259377P.

XX (HYBR-) HYBRIGENICS.

PA (CNRS) CENT NAT RECH SCI.

XX Legrain P; Marullo S; Jockers R;

XX WPI; 2002:583612/62.

DR N-PSDB; ABS51033.

XX

PT Novel complex of protein-protein interactions in adipocyte cells for
PT identifying compounds that modulate the protein-protein interactions and
XX useful for treating obesity and metabolic disorders.

PS Claim 1; Page 54; 125pp; English.

XX The invention relates to a complex of protein-protein interactions
CC (forming a protein-protein interaction map, PIM) in adipocyte cells as
CC defined in the specification, or polynucleotides in adipocytes encoding the
CC for the polypeptides. Also included are a recombinant cell expressing the
CC interacting polypeptides and a method of selecting a modulating compound
CC in adipocyte cells, by cultivating a recombinant host cell on a selective
CC medium containing a modulating compound and a reporter gene the
CC expression of which is toxic for the recombinant host cell which is
CC transformed with two vectors, where the first vector comprises a
CC polynucleotide encoding a first hybrid polypeptide and DNA binding domain
CC and the second vector comprising a polynucleotide encoding a second
CC hybrid polypeptide and an activating domain that activates the toxic
CC reporter gene, when the first and second hybrid polypeptides interact and
CC selecting the modulating compound which inhibits the growth of the
CC recombinant host cell (i.e. using the yeast two-hybrid system). The
CC complexes are useful for identifying compounds that modulate the protein-
CC protein interactions and useful for treating obesity and metabolic
CC disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The
CC compound isolated by the method is useful for treating and preventing of
CC obesity or metabolic diseases. The interactions between the proteins of
CC the complex further define a set of selected interacting domains, SID.
CC The present sequence represents a member of the protein complex of the
CC invention, used as the bait protein in the yeast two-hybrid assay

XX Sequence 770 AA;

Query Match 99.0%; Score 792; DB 5; Length 770;

Best Local Similarity 98.7%; Pred. No. 6.5e-76;

Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQHLQHSYDTPFMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60

DB 1 MAQWNLQQLDTRYLKQHLQHSYDTPFMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60

QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMPIARIVARCLWEESRLQTA 120

DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMPIARIVARCLWEESRLQTA 120

QY 121 TAAQGGQGANHPPTAAVVTKEQQLQHLQDVRRK 154

DB 121 TAAQGGQGANHPPTAAVVTKEQQLQHLQDVRRK 154

Search completed: May 5, 2005, 15:01:09

Job time : 50.8306 secs

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OM protein - protein search, using sw model

Run on: May 5, 2005, 14:55:35 ; Search time 23.1906 Seconds
(without alignments)
495.716 Million cell updates/sec

Title: US-10-090-185-8

Perfect score: 800

Sequence: 1 MAQWNQLQQLDTRYLKQLHQ.....AVTEKQOMLEQLQDVKR 154

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	800	100.0	154	3	US-09-387-418A-8
2	800	100.0	770	1	US-08-369-796-12
3	800	100.0	770	2	US-08-852-091-12
4	800	100.0	770	2	US-08-820-754-12
5	800	100.0	770	3	US-08-956-652-12
6	800	100.0	770	3	US-08-956-869-12
7	800	100.0	770	3	US-09-012-710-8
8	800	100.0	770	3	US-08-948-547-12
9	800	100.0	770	3	US-09-364-970-3
10	800	100.0	770	3	US-09-364-970-5
11	800	100.0	770	3	US-08-556-273-8
12	800	100.0	770	3	US-08-956-653A-12
13	800	100.0	770	4	US-08-212-185-12
14	800	100.0	770	5	PCT-US95-17025-12
15	792	99.0	770	1	US-08-416-581B-1
16	792	99.0	770	1	US-08-416-581B-5
17	792	99.0	770	1	US-08-416-581B-9
18	792	99.0	770	3	US-03-087-465-6
19	792	99.0	770	3	US-09-526-542-2
20	792	99.0	770	4	US-09-972-800A-6
21	792	99.0	770	4	US-10-117-087-2
22	792	99.0	771	1	US-08-276-099A-14
23	792	99.0	771	1	US-08-781-890-14
24	380	47.5	154	3	US-09-387-418A-11
25	380	47.5	712	1	US-08-369-796-6
26	380	47.5	712	2	US-08-852-091-6
27	380	47.5	712	2	US-08-820-754-6

28	380	47.5	712	3	US-08-956-652-6	Sequence 6, Appli
29	380	47.5	712	3	US-08-956-869-6	Sequence 6, Appli
30	380	47.5	712	3	US-08-948-547-6	Sequence 6, Appli
31	380	47.5	712	3	US-08-956-653A-6	Sequence 6, Appli
32	380	47.5	712	4	US-08-212-185-6	Sequence 2, Appli
33	380	47.5	712	4	US-09-430-806A-2	Sequence 6, Appli
34	380	47.5	712	5	PCT-US95-17025-6	Sequence 6, Appli
35	380	47.5	729	4	US-09-917-254-97	Sequence 97, Appli
36	380	47.5	740	1	US-08-276-099A-12	Sequence 12, Appli
37	380	47.5	740	1	US-08-781-890-12	Sequence 12, Appli
38	380	47.5	750	1	US-08-369-796-4	Sequence 4, Appli
39	380	47.5	750	2	US-08-852-091-4	Sequence 4, Appli
40	380	47.5	750	2	US-08-820-754-4	Sequence 4, Appli
41	380	47.5	750	3	US-08-956-652-4	Sequence 4, Appli
42	380	47.5	750	3	US-08-956-869-4	Sequence 4, Appli
43	380	47.5	750	3	US-08-948-547-4	Sequence 4, Appli
44	380	47.5	750	3	US-09-087-465-2	Sequence 2, Appli
45	380	47.5	750	3	US-09-364-970-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-387-418A-8

; Sequence 8, Application US/09387418A

; Patent No. 6391572

; GENERAL INFORMATION:

; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzieszczyńska, Melissa H

; APPLICANT: Horvath, Curt M

; APPLICANT: Darnell Jr., James E

; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

; TITLE OF INVENTION: INTERACTIONS

; FILE REFERENCE: 600-1-253

; CURRENT APPLICATION NUMBER: US/09/387,418A

; CURRENT FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 8

; LENGTH: 154

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-387-418A-8

Query Match 100.0%; Score 800; DB 3; Length 154;

Best Local Similarity 100.0%; Pred. No. 7.3e-79;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDTFPMEIURQFLAPWIESQDWAYAAKESHATLVFHNL 60

Db 1 MAQWNQLQQLDTRYLKQLHOLYSDTFPMEIURQFLAPWIESQDWAYAAKESHATLVFHNL 60

Qy 61 LGEDIQOYSFLOESNVLYOHNLRRIRKQFLQSRVLEKPMETIARIVARCLWESRLLQTA 120

Db 61 LGEDIQOYSFLOESNVLYOHNLRRIRKQFLQSRVLEKPMETIARIVARCLWESRLLQTA 120

Qy 121 TAAQGGQANHPHTAAVVTEKQOMLEQLQDVKR 154

Db 121 TAAQGGQANHPHTAAVVTEKQOMLEQLQDVKR 154

RESULT 2

US-08-369-796-12

; Sequence 12, Application US/08369796

; Patent No. 5716622

; GENERAL INFORMATION:

; APPLICANT: James E. Darnell, Jr.

; APPLICANT: Zilong Wen

; APPLICANT: Curt M. Horvath

; APPLICANT: Zhong Zhong

; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL

; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS

```
;
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-369-796-12

Query Match 100.0%; Score 800; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
QY 61 LGEDIQQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEDIQQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQANHPTAAVVTKEQKQMLEQHLQDVVRK 154
Db 121 TAAQGGQANHPTAAVVTKEQKQMLEQHLQDVVRK 154

RESULT 3
US-08-852-091-12
; Sequence 12, Application US/08852091
; Patent No. 5883228
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,091
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-852-091-12

Query Match 100.0%; Score 800; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMELRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
QY 61 LGEDIQQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEDIQQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQANHPTAAVVTKEQKQMLEQHLQDVVRK 154
Db 121 TAAQGGQANHPTAAVVTKEQKQMLEQHLQDVVRK 154

RESULT 4
US-08-820-754-12
; Sequence 12, Application US/08820754
; Patent No. 5976835
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,754
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
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; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-820-754-12

Query Match 100.0%; Score 800; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVPHNL 60
DB 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVPHNL 60

QY 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
DB 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

QY 121 TAAQGGQANHPTAAVTEKQMLEQHLQDVKR 154
DB 121 TAAQGGQANHPTAAVTEKQMLEQHLQDVKR 154

RESULT 5
US-08-956-652-12
; Sequence 12, Application US/08956652
; Patent No. 6013475
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,652
; FILING DATE:
; CLASSIFICATION:

; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-956-652-12

Query Match 100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVPHNL 60
DB 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAAKESHATLVPHNL 60

QY 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
DB 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

QY 121 TAAQGGQANHPTAAVTEKQMLEQHLQDVKR 154
DB 121 TAAQGGQANHPTAAVTEKQMLEQHLQDVKR 154

RESULT 6
US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,652
; FILING DATE:
; CLASSIFICATION:
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APPLICATION NUMBER: US/08/956,869
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/212,185
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/854,296
 FILING DATE: 19-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO US93/02569
 FILING DATE: 19-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/136,588
 FILING DATE: 24-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 770 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-956-869-12

Query Match	100.0%;	Score 800;	DB 3;	Length 770;
Best Local Similarity	100.0%;	Pred. No. 5.9e-78;		
Matches 154; Conservative	0;	Mismatches 0;	Indels 0;	

1	MAQWNLQGLDTRYIKQLHQLYSDTPEMLRQFLAPWIESQDWAYAASKESHATLVPHNL	60
	Db	
1	MAQWNLQGLDTRYIKQLHQLYSDTPEMLRQFLAPWIESQDWAYAASKESHATLVPHNL	60
	Db	
61	LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSYLEKPKMEIARIVARCLWEESRLTAA	120
	Db	
61	LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSYLEKPKMEIARIVARCLWEESRLTAA	120
	QY	
121	TAAQCGGQANHPTAAVVVTEKQMLEHQLQDVRRK	154
	Db	
121	TAAQCGGQANHPTAAVVVTEKQMLEHQLQDVRRK	154
	Db	

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RESULT 7
US-09-012-710-8
; Sequence 8, Application US/09012710
; Patent No. 6087478
;
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe.
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/09/012,710
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq., David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 600-1-194
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-487-5800
/ TELEFAX: 201-343-1684
/ TELEX: 133521
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 770 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ US-09-012-710-8

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Query Match      100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1	MAQNNQLCOOLDTRYLKQLHOLYSDTFMPELROFLAPMIESQDWAYAASKESHATLVFPHNL	60
	1	MAQNNQLCOOLDTRYLKQLHOLYSDTFMPELROFLAPMIESQDWAYAASKESHATLVFPHNL
		60
61	LGEIDQOQSYRFLQSQNVLYQHNLRIIKFTLOSRYLEKPEMELIARIVARCLWEESRLLOTAA	120
	61	LGEIDQOQSYRFLQSQNVLYQHNLRIIKFTLOSRYLEKPEMELIARIVARCLWEESRLLOTAA
		120
121	TAAQGGQGANHTAAVVTKEQOMLEQHLQDVVRKR	154
	121	TAAQGGQGANHTAAVVTKEQOMLEQHLQDVVRKR
		154

RESULT 8
 US-08-948-547-12
 ; Sequence 12, Application US/08948547
 ; Patent No. 6124118
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan
 ; APPLICANT: Wen, Zilong
 ; APPLICANT: Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/948,547
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/212,185
 ; FILING DATE: 11-MAR-1994
 ; APPLICATION NUMBER: US 07/980,498
 ; FILING DATE: 23-NOV-1992
 ; PRIOR APPLICATION DATA:
 ;

APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12

Query Match 100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHL 60
Db 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHL 60

Qy 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154

RESULT 9
US-09-364-970-3
Sequence 3, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-3

Query Match 100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHL 60
Db 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHL 60

Qy 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154

APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12

Query Match 100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHL 60
Db 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHL 60

Qy 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154

APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12

Query Match 100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHL 60
Db 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHL 60

Qy 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154

Qy 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154

RESULT 10
US-09-364-970-5
Sequence 5, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-5

Query Match 100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHL 60
Db 1 MAQWNQLQQLDTRYLKQLHOLYSDFPMELRQFLAPWIESQDWAYAASKESHATLVFPHL 60

Qy 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQANHPHTAAVVTKEQOMLEQHLQDVRRK 154

RESULT 11
US-09-556-273-8
Sequence 8, Application US/09556273
Patent No. 6312887
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Darneil, Jr., James E.
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,273
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,710
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-556-273-8

Query Match 100.0%; Score 800; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAAASKESHATLVFHNL 60
DB 1 MAQWNQLQQLDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAAASKESHATLVFHNL 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
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QY 121 TAAQGGQANHPHTAAVVTKEQMLQHLQDVRRK 154
DB 121 TAAQGGQANHPHTAAVVTKEQMLQHLQDVRRK 154

RESULT 12
US-08-956-653A-12
Sequence 12, Application US/08956653A
Patent No. 6338949
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
MISMATCHES: 0; Mismatches 0; Indels 0; Gaps 0;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAAASKESHATLVFHNL 60
DB 1 MAQWNQLQQLDTRYLKQLHQLYSDFPFMELRQFLAPWIESQDWAYAAASKESHATLVFHNL 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQANHPHTAAVVTKEQMLQHLQDVRRK 154
DB 121 TAAQGGQANHPHTAAVVTKEQMLQHLQDVRRK 154

RESULT 13
US-08-212-185-12
Sequence 12, Application US/08212185
Patent No. 6605442
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-17025-12
; US-08-212-185-12

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Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQANHPHTAAVVTXKQMLEQHLQDVKR 154
Db 121 TAAQGGQANHPHTAAVVTXKQMLEQHLQDVKR 154

RESULT 14
PCT-US95-17025-12
; Sequence 12, Application PC/TUS9517025
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17025
; FILING DATE: 28-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
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; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-17025-12

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Best Local Similarity 100.0%; Pred. No. 5.9e-78;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
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RESULT 15
US-08-416-581B-1
; Sequence 1, Application US/08416581B
; Patent No. 5719042
; GENERAL INFORMATION:
; APPLICANT: Kishimoto, Tadamoto
; APPLICANT: Akira, Shizuo
; TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,581B
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-65825/1994
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: Q-37891
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-416-581B-1
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Query Match      99.0%; Score 792; DB 1; Length 770;
Best Local Similarity 98.7%; Pred. No. 4.3e-77;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Search completed: May 5, 2005, 14:58:51
Job time : 26.1906 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2005, 14:59:00 ; Search time 64.8612 Seconds
(without alignments)
792.064 Million cell updates/sec

Title: US-10-090-185-8
Perfect score: 800
Sequence: 1 MAQWNQLQDLTRYLKQLH.....AVTEKQOMLEQHLQDVQRK 154

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	800	100.0	770	11	US-09-876-773-6
3	800	100.0	770	14	US-10-045-792-8
4	800	100.0	770	17	US-10-639-617-12
5	792	99.0	720	15	US-10-380-020-4
6	792	99.0	769	15	US-10-380-020-2
7	792	99.0	769	15	US-10-380-020-5
8	792	99.0	770	14	US-10-038-010-56
9	792	99.0	770	14	US-10-117-087-2
10	792	99.0	770	15	US-10-116-275-329
11	792	99.0	770	15	US-10-116-275-349
12	792	99.0	793	9	US-09-925-302-780
13	792	99.0	793	10	US-09-925-302-780

14	380	47.5	154	13	US-10-090-185-11	Sequence 11, Appl
15	380	47.5	712	11	US-09-876-773-6	Sequence 6, Appl
16	380	47.5	712	14	US-10-245-120-2	Sequence 2, Appl
17	380	47.5	712	17	US-10-639-617-6	Sequence 6, Appl
18	380	47.5	712	17	US-10-936-390-5	Sequence 5, Appl
19	380	47.5	750	9	US-09-833-205-2	Sequence 2, Appl
20	380	47.5	750	11	US-09-876-773-4	Sequence 4, Appl
21	380	47.5	750	14	US-10-245-120-1	Sequence 1, Appl
22	380	47.5	750	14	US-10-308-279-44	Sequence 44, Appl
23	380	47.5	750	16	US-10-755-889-352	Sequence 352, App
24	380	47.5	750	16	US-10-755-889-823	Sequence 823, App
25	380	47.5	750	17	US-10-492-043-19	Sequence 19, Appl
26	380	47.5	750	17	US-10-639-617-4	Sequence 4, Appl
27	380	47.5	786	9	US-09-925-297-550	Sequence 550, App
28	378	47.2	749	9	US-09-833-205-4	Sequence 6, Appl
29	378	47.2	749	9	US-09-833-205-6	Sequence 8, Appl
30	378	47.2	749	11	US-09-876-773-8	Sequence 7, Appl
31	378	47.2	749	14	US-10-045-792-7	Sequence 39, Appl
32	378	47.2	749	14	US-10-205-194-39	Sequence 8, Appl
33	378	47.2	749	17	US-10-639-617-8	Sequence 4, Appl
34	360	45.0	131	14	US-10-245-120-4	Sequence 10, Appl
35	334.5	41.8	748	11	US-09-876-773-10	Sequence 10, Appl
36	334.5	41.8	748	17	US-10-639-617-10	Sequence 9, Appl
37	334.5	41.8	749	14	US-10-045-792-9	Sequence 437, App
38	333.5	41.7	423	14	US-10-177-293-437	Sequence 439, App
39	333.5	41.7	748	14	US-10-177-293-439	Sequence 70, Appl
40	333.5	41.7	748	16	US-10-755-889-70	Sequence 389, App
41	333.5	41.7	748	16	US-10-755-889-362	Sequence 2, Appl
42	247.5	30.9	532	14	US-10-205-823-389	Sequence 2, Appl
43	247.5	30.9	851	11	US-09-876-773-2	Sequence 2, Appl
44	247.5	30.9	851	14	US-10-045-792-2	Sequence 2, Appl
45	247.5	30.9	851	15	US-10-179-451-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-090-185-8
; Sequence 8, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR E
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-8

Query Match 100.0%; Score 800; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. NO. 4.7e-77;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNQLQDLTRYLKQLHQLYSDTFPMEARQFLAPWIESQDWAYAAKESHATLVFHNL 60
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Db 61 LGEIDQYSRFLQBSNVLYQHNLRRIKQFLQSRVLEKPMETARIVARCLWEESRLQTAA 120

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Db 121 TAAQGGQANHPTAAVVTETKQMLQHLQDVRKR 154

RESULT 2
US-09-876-773-12
; Sequence 12, Application US/09876773
; Publication No. US20040058318A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,773
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US/07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US/07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match 100.0%; Score 800; DB 11; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.7e-76;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 LGEDIQYSRFLOESNVLYQHNLRRIKQFLQSRVLEKPMETARIVARCLWEESRLLOTA 120

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US-10-045-792-8
; Sequence 8, Application US/10045792
; Publication No. US20030003563A1
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; Moarefi, Ismail
; Darnell, Jr., James E.
; Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,792
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8

Query Match 100.0%; Score 800; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.7e-76;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAQNNQLQQLDTRYLKHQLHLYSDTTPMELRQFLAPWIESQDWAYAASKESHATLVFHN 60
Db 1 MAQNNQLQQLDTRYLKHQLHLYSDTTPMELRQFLAPWIESQDWAYAASKESHATLVFHN 60
Qy 61 LGEDIQYSRFLOESNVLYQHNLRRIKQFLQSRVLEKPMETARIVARCLWEESRLLOTA 120
Db 61 LGEDIQYSRFLOESNVLYQHNLRRIKQFLQSRVLEKPMETARIVARCLWEESRLLOTA 120
Qy 121 TAAQGGQANHPTAAVVTETKQMLQHLQDVRKR 154
Db 121 TAAQGGQANHPTAAVVTETKQMLQHLQDVRKR 154

RESULT 4

US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/639,617
; FILING DATE: 12-Aug-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

Query Match 100.0%; Score 800; DB 17; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.7e-76;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAQWNLQQLDTRYLKQLHQLYSDFPFMEIRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
Db 1 MAQWNLQQLDTRYLKQLHQLYSDFPFMEIRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
Qy 61 LGEIDQOYSRFLQESNVLYOHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYOHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Qy 121 TAAQCGQANHPTAAVVTKEQKMLEQHLQDVRRK 154
Db 121 TAAQCGQANHPTAAVVTKEQKMLEQHLQDVRRK 154

RESULT 5

US-10-380-020-4
; Sequence 4, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-4

Query Match 99.0%; Score 792; DB 15; Length 720;
Best Local Similarity 98.7%; Pred. No. 2.4e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNLQQLDTRYLKQLHQLYSDFPFMEIRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
Db 1 MAQWNLQQLDTRYLKQLHQLYSDFPFMEIRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
Qy 61 LGEIDQOYSRFLQESNVLYOHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYOHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Qy 121 TAAQCGQANHPTAAVVTKEQKMLEQHLQDVRRK 154
Db 121 TAAQCGQANHPTAAVVTKEQKMLEQHLQDVRRK 154

RESULT 6

US-10-380-020-2
; Sequence 2, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 769
; TYPE: PRT<
; ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match 99.0%; Score 792; DB 15; Length 769;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNLQQLDTRYLKQLHQLYSDFPFMEIRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
Db 1 MAQWNLQQLDTRYLKQLHQLYSDFPFMEIRQFLAPWIESQDWAYAAKESHATLVFPHNL 60
Qy 61 LGEIDQOYSRFLQESNVLYOHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Db 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154

RESULT 7
US-10-380-020-5
; Sequence 5, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-5

Query Match 99.0%; Score 792; DB 15; Length 769;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVPHNL 60

QY 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

QY 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154

RESULT 8
US-10-038-010-56
; Sequence 56, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 56
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: STAT3 : Transcription factor
; LOCATION: (1)..(770)
; OTHER INFORMATION:
US-10-038-010-56

Query Match 99.0%; Score 792; DB 14; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVPHNL 60

QY 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

QY 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154

RESULT 9
US-10-117-087-2
; Sequence 2, Application US/10117087
; Publication No. US20030166854A1
; GENERAL INFORMATION:
; APPLICANT: SERLUPI-CRESCENZI, Ottaviano
; APPLICANT: DELLA PIETRA, Linda
; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
; FILE REFERENCE: SERLUPI=2
; CURRENT APPLICATION NUMBER: US/10/117,087
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/526,542
; PRIOR FILING DATE: 2000-03-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Human
US-10-117-087-2

Query Match 99.0%; Score 792; DB 14; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNQLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVPHNL 60

QY 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

QY 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHTAAVVTKEQOMLEQHLQDVRRK 154

RESULT 10
US-10-116-275-329
; Sequence 329, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Eian Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: Patent in version 3.1

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; SEQ ID NO 329
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Rat
US-10-116-275-329

Query Match          99.0%; Score 792; DB 15; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAOWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVFHN 60
Db 1 MAOWNLQQLDTRYLYEQHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVFHN 60

Qy 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154

RESULT 11
US-10-116-275-349
; Sequence 349, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 349
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-349

Query Match          99.0%; Score 792; DB 15; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.7e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAOWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVFHN 60
Db 1 MAOWNLQQLDTRYLYEQHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVFHN 60

Qy 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

Qy 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154
Db 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154

RESULT 12
US-09-925-302-780
; Sequence 780, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
```

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; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match          99.0%; Score 792; DB 9; Length 793;
Best Local Similarity 98.7%; Pred. No. 2.8e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAOWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVFHN 60
Db 24 MAOWNLQQLDTRYLYEQHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVFHN 83

Qy 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 84 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 143

Qy 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154
Db 144 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 177

RESULT 13
US-09-925-302-780
; Sequence 780, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match          99.0%; Score 792; DB 10; Length 793;
Best Local Similarity 98.7%; Pred. No. 2.8e-75;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAOWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVFHN 60
Db 24 MAOWNLQQLDTRYLYEQHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVFHN 83

Qy 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
Db 84 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 143

Qy 121 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 154
Db 144 TAAQGGQGANHPTAAVVTXKQMLEQHLQDVRRK 177

RESULT 14
US-10-090-185-11
; Sequence 11, Application US/10090185
; Publication No. US20020197647A1
```

GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wzesczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
PRIORITY FILING DATE: 2002-03-04
PRIORITY FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 11
LENGTH: 154
TYPE: PRT
ORGANISM: Mus musculus
US-10-090-185-11

Query Match 47.5%; Score 380; DB 13; Length 154;
Best Local Similarity 44.8%; Pred. No. 2.5e-32;
Matches 69; Conservative 42; Mismatches 41; Indels 2; Gaps 1;

Qy 1 MAQNNQLQDLTRYLKHQHYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Db 1 MSQWYELQQLDQSKFLQVHLYDSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Qy 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 120
Db 61 LSQDDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 120
Qy 121 TAAQGGQANHTAAVVTKEQOMLEQHLQDVVRK 154
Db 121 RFNQ--AQSGNIQSTVMDKQKELDSKVRNVKDK 152

RESULT 15

US-09-876-773-6
Sequence 6, Application US/09876773
Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US/07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US/07/854,296
FILING DATE: 19-MAR-1992

APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 712 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-876-773-6

Query Match 47.5%; Score 380; DB 11; Length 712;
Best Local Similarity 44.8%; Pred. No. 1.18e-31;
Matches 69; Conservative 42; Mismatches 41; Indels 2; Gaps 1;

Qy 1 MAQNNQLQDLTRYLKHQHYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Db 1 MSQWYELQQLDQSKFLQVHLYDSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Qy 61 LGEIDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 120
Db 61 LSQDDQYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 120
Qy 121 TAAQGGQANHTAAVVTKEQOMLEQHLQDVVRK 154
Db 121 RFNQ--AQSGNIQSTVMDKQKELDSKVRNVKDK 152

Search completed: May 5, 2005, 15:17:40
Job time : 65.8612 secs

A;Molecule type: mRNA

A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P42227; GB:L292278; NID:G476715; PIDN:AAA37254.1; PID:G476716
R;Yamamoto, K.; Quille, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, J.E.; Levy, D.E.
J. Biol. Chem. 269, 24391-24395, 1994
A;Title: Acute phase response factor and additional members of the interferon-stimulated
A;Reference number: I49009; MUID:95014185; PMID:7523373
A;Accession: I49009
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-393, M, 395-700, 702-770 <RE2>
A;Cross-references: EMBL:U08378; NID:G473889; PIDN:AAA56668.1; PID:G473890
C;Genetics:
A;Gene: APRF
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 99.0%; Score 792; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 1.1e-61;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNLQQLDTRYLKQHLQYSDTPFMEIRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Db 1 MAQWNLQQLDTRYLEQHLQYSDSPFMEIRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Qy 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTA 120
Db 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTA 120
Qy 121 TAAQGGQANHTAAVTEKQMLEQHLQDV 154
Db 121 TAAQGGQANHTAAVTEKQMLEQHLQDV 154

RESULT 3
A46159
interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Improt, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG
A;Reference number: A46159; MUID:92366557; PMID:1502203
A;Accession: A46159
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
A;Cross-references: UNIPROT:P42224
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 47.5%; Score 380; DB 2; Length 739;
Best Local Similarity 44.8%; Pred. No. 1.5e-25;
Matches 69; Conservative 42; Mismatches 41; Indels 2; Gaps 1;

Qy 1 MAQWNLQQLDTRYLKQHLQYSDTPFMEIRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Db 1 MSQWYELQQLDQSKLEQVHLYDSDPFMEIRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Qy 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTA 120
Db 61 LSQLDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTA 120
Qy 121 TAAQGGQANHTAAVTEKQMLEQHLQDV 154
Db 121 RFNQ--AQSGNIQSTVMDKQKELDSKVRNVDK 152

RESULT 4
A56047
gamma-interferon activation site-binding protein Stat4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C;Accession: A56047
R;Yamamoto, K.; Quille, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, J.E.; Levy, D.E.
Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in ear
A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-748 <YAM>
A;Cross-references: UNIPROT:P42228; GB:U09351; NID:G509502; PIDN:AAA19692.1; PID:G509503
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein

Query Match 41.8%; Score 334.5; DB 2; Length 748;
Best Local Similarity 41.4%; Pred. No. 1.5e-21;
Matches 63; Conservative 38; Mismatches 50; Indels 1; Gaps 1;

Qy 1 MAQWNLQQLDTRYLKQHLQYSDTPFMEIRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Db 1 MSQWNLQQLDTRYLKQHLQYSDTPFMEIRQFLAPWIESQDWAYAASKESHATLVFHNL 60
Qy 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTA 120
Db 61 LQIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTA 120
Qy 121 TAAQGGQANHTAAVTEKQMLEQHLQDV 152
Db 121 NMPIQGLEKSLQSSSVSRQRNVEHKVSAIK 151

RESULT 5
A46160
interferon alpha-induced transcription activator ISGF-3, 113K chain - human
N;Alternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
R;Fu, X.Y.; Schindler, C.; Improt, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator,
A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-851 <FU>
A;Cross-references: UNIPROT:P52630
A;Note: sequence extracted from NCBI backbone (NCBIP:110820)
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
submitted to the EMBL Data Library, December 1994
A;Reference number: S71908
A;Accession: S71908
A;Molecule type: DNA
A;Residues: 1-851 <YAN>
A;Cross-references: EMBL:U18671; NID:G1293919; PIDN:AAA98760.1; PID:G1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in
A;Reference number: S53873; MUID:95192056; PMID:7885841
A;Accession: S53873
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-196;392-591;684-730 <YAN>
A;Cross-references: EMBL:U18671
C;Genetics:
A;Gene: stat2
A;Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; 40/2;
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: signal transduction; transcription regulation

Query Match 30.9%; Score 247.5; DB 2; Length 851;
Best Local Similarity 37.6%; Pred. No. 7.5e-14;
Matches 59; Conservative 34; Mismatches 55; Indels 9; Gaps 6;

```
Qy 1 MAQWNLQQLDTRYLKQHLQYSDT-PPMELRQFLAPWIESQDWAYAA--SKESHATLVF 57
Db 1 MAQWNLQQLDTRYLKQHLQYSDT-PPMELRQFLAPWIESQDWAYAA--SKESHATLVF 60
Qy 58 HNLGELIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELRQFLAPWIESQDWAYAA--ASKESHATLV 116
Db 61 FHFLDQNLQYECGRSCQDPESLLOHNLKFKCRDQIP-FSQDPTQLAEMIFNLLLEEKRL 119
Qy 117 QTAATAAQCGQGANHPHTAAVVTEKQ-MLEQHLQDVR 152
Db 120 IQAORAQLEQGE---PVLETPVESQOHEIESRIILDLR 153

RESULT 6
149274
mammary gland factor - mouse
N;Alternate names: STAT5 protein homolog p80
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49274; S54773; S54727
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved i
A;Reference number: I49273; MUID:96004632; PMID:7568026
A;Accession: I49274
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-786 <RES>
A;Cross-references: UNIPROT:P42232; UNIPROT:O9JWK1; EMBL:U21110; NID:g747973; PIDN:AAC52
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Accession: S54773
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-432,'E',434-786 <MUI>
A;Cross-references: EMBL:I248539; NID:g758635; PIDN:CAA88420.1; PID:g758636
R;Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,
EMBO J. 14, 1402-1411, 1995
A;Title: Interleukin-3 signals through multiple isoforms of Stat5.
A;Reference number: S54725; MUID:95246733; PMID:7537213
A;Accession: S54727
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-432,'E',434-786 <AZA>
C;Genetics:
A;Gene: Stat5b
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 23.5%; Score 188; DB 2; Length 786;
Best Local Similarity 30.1%; Pred. No. 1.1e-08;
Matches 47; Conservative 26; Mismatches 75; Indels 8; Gaps 2;

Qy 1 MAQWNLQQLDTRYLKQHLQYSDT-PPMELRQFLAPWIESQDWAYAA--ASKESHATLV 56
Db 1 MAMWIAQQLQGDALRQMVLYGQHFPIEVRYHLYAQMIESQPDALDLDNPDQRAQATOL 60
Qy 57 FHNLLGELIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELRQFLAPWIESQDWAYAA--ASKESHATLV 116
Db 61 LEGVLQELQKKAHQVGDGFLKIKLGHVATQYQSTYDRCPMELVRCIRHILYNEORLV 120
Qy 117 QTAATAAQCGQGANHPHTAAVVTEKQMLEQHLQDVR 152
Db 121 REANNSSPAGS---LADAMSQKHLOINQTFEELR 152

RESULT 7
G02317
transcription activator stat5a - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02317
```

```
R;Lin, J.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:gl151169; PIDN:AAB06589.1; PID:gl15
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 23.4%; Score 187; DB 2; Length 794;
Best Local Similarity 31.4%; Pred. No. 1.4e-08;
Matches 48; Conservative 23; Mismatches 68; Indels 14; Gaps 3;

Qy 1 MAQWNLQQLDTRYLKQHLQYSDT-PPMELRQFLAPWIESQDWAYAA--ASKESHATLV 56
Db 1 MAGWIAQQLQGDALRQMVLYGQHFPIEVRYHLYAQMIESQPDALDLDNPDQRAQATOL 60
Qy 57 FHNLLGELIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELRQFLAPWIESQDWAYAA--ASKESHATLV 116
Db 61 LEGVLQELQKKAHQVGDGFLKIKLGHVATQYQSTYDRCPMELVRCIRHILYNEORLV 120
Qy 117 QTAATAAQCGQGANHPHTAAVVTEKQMLEQHLQ 149
Db 121 REA-----NNCSPAGILV---DAMSQKHLO 143

RESULT 8
S54772
mammary gland factor - mouse
N;Alternate names: stat5 protein
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54772; I49273
R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Accession: S54772
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-793 <MUI>
A;Cross-references: UNIPROT:P42230; UNIPROT:O9JJA0; EMBL:I248538; NID:g758633; PIDN:CAA88
R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved i
A;Reference number: I49273; MUID:96004632; PMID:7568026
A;Accession: I49273
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-793 <RES>
A;Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972
C;Genetics:
A;Gene: Stat5a
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 23.2%; Score 186; DB 2; Length 793;
Best Local Similarity 29.5%; Pred. No. 1.7e-08;
Matches 46; Conservative 26; Mismatches 76; Indels 8; Gaps 2;

Qy 1 MAQWNLQQLDTRYLKQHLQYSDT-PPMELRQFLAPWIESQDWAYAA--ASKESHATLV 56
Db 1 MAGWIAQQLQGDALRQMVLYGQHFPIEVRYHLYAQMIESQPDALDLDNPDQRAQATOL 60
Qy 57 FHNLLGELIDQOYSRFLQESNVLYQHNLRRIRKQFLQSRYLEKPMELRQFLAPWIESQDWAYAA--ASKESHATLV 116
Db 61 LEGVLQELQKKAHQVGDGFLKIKLGHVATQYQSTYDRCPMELVRCIRHILYNEORLV 120
Qy 117 QTAATAAQCGQGANHPHTAAVVTEKQMLEQHLQDVR 152
Db 121 REANNSSPAG---VLVDAMSQKHLOINQTFEELR 152
```



```
QY 133 TAAVTEKQMLEQHLQD 150
Db 168 TPANGTGPSEALAMLOE 185

RESULT 13
T22552
hypothetical protein ZK1151.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T22552; T27703
R:Harris, B.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19580
A:Accession: T22552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1355 <WIL>
A:Cross-references: EMBL:Z92788; PIDN:CA807214.1; GSPDB:GN00019; CESP:ZK1151.1
A:Experimental source: clone F53B8
R:Harris, B.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z20408
A:Accession: T27703
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1355 <W12>
A:Cross-references: EMBL:Z93398; PIDN:CA807724.1; GSPDB:GN00019; CESP:ZK1151.1
A:Experimental source: clone ZK1151
C:Genetics:
A:Gene: CESP:ZK1151.1
A:Map position: 1
A:Introns: 94/3; 124/3; 150/3; 209/3; 248/3; 311/3; 424/3; 734/2; 934/2; 1104/3; 1167/3;

Query Match 11.0%; Score 88; DB 2; Length 1355;
Best Local Similarity 25.3%; Pred. No. 13;
Matches 4; Conservative 25; Mismatches 57; Indels 42; Gaps 10;

QY 4 WNQLQLD---TRYLKQ-LHQL-----YSD-----TFPMELQFLA 35
Db 677 WSDIKQLDPLMTNYKQLLHEMELREKQYNDVHNGAALLNQGHPAIRVIEVLRQMS 736

QY 36 PWIESQWAYAASK--ESHA--TLVFHNLGEIDQYSRFLQESNVLYQHNLRIKQFLQ 91
Db 737 QW-----DWLLALSCLBEHLRDALNLKSFMEASDA-EAWTQGSVRLNNYNTDFSL 791

QY 92 --SRYLEKPMELIARIVARCLWEESRLQTAATAA---QOQGOANHP 132
Db 792 EGERFLELDEIKELNKYHQVLMALTEKASISPLWQGRGRIHPH 837

RESULT 14
T40287
hypothetical protein SPBC354.07c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40287
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21918
A:Accession: T40287
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-371 <WOO>
A:Cross-references: EMBL:AL022071; PIDN:CAA17807.1; GSPDB:GN00067; SPDB:SPBC354.07c
A:Experimental source: strain 972h-; cosmid c354
C:Genetics:
A:Gene: SPDB:SPBC354.07c
A:Map position: 2
A:Introns: 8/2; 75/3

Query Match 10.3%; Score 82.5; DB 2; Length 371;
Best Local Similarity 24.0%; Pred. No. 8.4;
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```
Matches 44; Conservative 31; Mismatches 57; Indels 51; Gaps 9;
QY 5 NQLQQLDTRYLKQHLQYSDTFP---MELRQFLAPWIESQDWAYAASKESHATLVFHNLL 61
Db 147 NQLQQLRV-HLEKYNETYITLNPISLEGWFWAPYIELYGVSTIVSVNTVITKIDYSGR 205

QY 62 GEIDQYSRFLQES--NVLYQHN-----LRRIKQFLQSRYLE-- 96
Db 206 G-----YFRGTRKNSFKATIFEKNEPDYIIEGVWGTGSKLTIPSLKSTIFPLSPLEAT 260

QY 97 ---KP-METARIVARCLWEESRLQTAATAAQGGQANHPATAAVVTEKQQLMLQHLQDV 151
Db 261 PITVKPESEMGDWESRNWKE-----VSAALASGNVD-----IVSKKSTIEQSQRDM 308

QY 152 RKR 154
Db 309 RKK 311

RESULT 15
F71884
probable lipopolysaccharide biosynthesis protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: F71884
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho-
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: F71884
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-373 <ARN>
A:Cross-references: UNIPROT:Q9ZKWA; GB:AE001511; GB:AE001439; NID:g4155382; PIDN:RAD0639
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0820

Query Match 10.3%; Score 82.5; DB 2; Length 373;
Best Local Similarity 33.8%; Pred. No. 8.4;
Matches 27; Conservative 14; Mismatches 26; Indels 13; Gaps 5;

QY 18 LHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQYSRFLQESNV 77
Db 287 LH-FYADEKPV--KHFGYPY--SKEWHQVAFKTSFESLVFENLVGKIE---TFTE---- 333

QY 78 LYQHNLRIKQFLQSRYLEK 97
Db 334 LNDHNKKSPFEFLNRLNKK 353

Search completed: May 5, 2005, 15:01:50
Job time : 18.2329 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 14:55:35 ; Search time 41.6706 Seconds
(without alignments)
1892.467 Million cell updates/sec

Title: US-10-090-185-8
Perfect score: 800
Sequence: 1 MAQWNLQDLTRYLKQLHQ.....AVVTEKQMLQHLQDVQRK 154

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	792	99.0	770	1 STA3 HUMAN	P40763 homo sapien
2	792	99.0	770	1 STA3 MOUSE	P42227 mus musculus
3	792	99.0	770	1 STA3 RAT	P52631 rattus norv
4	786	98.2	770	1 STA3 BOVIN	P61635 bos taurus
5	779	97.4	771	2 Q6DV79	Q6dv79 gallus gall
6	760	95.0	769	2 Q9PVX8	Q9pvx8 xenopus lae
7	749	93.6	766	2 Q7ZXK3	Q7zxk3 xenopus lae
8	694.5	86.8	414	2 Q7ZTS5	Q7zts5 brachydanio
9	694.5	86.8	786	2 Q6NV46	Q6nv46 brachydanio
10	694.5	86.8	806	2 Q93599	Q93599 brachydanio
11	691.5	86.4	767	2 O13133	O13133 oncorhynch
12	685.5	85.7	765	2 Q6DVF3	Q6dvf3 oryzias lat
13	685.5	85.7	785	2 Q6GUE7	Q6gue7 oryzias lat
14	681.5	85.2	764	2 Q90Y16	Q90y16 tetraodon f
15	401	50.1	751	2 Q8JGNO	Q8jgn0 xenopus lae
16	380	47.5	750	1 STA1 HUMAN	P42224 homo sapien
17	380	47.5	750	2 Q68D00	Q68d00 homo sapien
18	379	47.4	712	2 Q6PEQ7	Q6peq7 rattus norv
19	379	47.4	1165	2 Q7TP57	Q7tp57 rattus norv
20	378	47.2	712	2 Q99K94	Q99k94 mus musculus
21	378	47.2	749	1 STA1 MOUSE	P42225 mus musculus
22	378	47.2	749	2 Q8C3V4	Q8c3v4 mus musculus
23	378	47.2	749	2 Q8C497	Q8c497 mus musculus
24	378	47.2	749	2 Q9D323	Q9d323 mus musculus
25	378	47.2	749	2 Q9QXK0	Q9qxk0 rattus norv
26	378	47.2	755	2 Q8C8M3	Q8c8m3 mus musculus
27	378	47.2	757	2 Q764M5	Q764m5 sus scrofa
28	354.5	44.3	758	2 Q90Y17	Q90y17 tetraodon f
29	351	43.9	754	2 O13132	O13132 oncorhynch
30	346	43.2	754	2 O13131	O13131 oncorhynch
31	336.5	42.1	718	2 Q801Y2	Q801y2 carassius a

RESULT 1

ID	STA3 HUMAN	STANDARD;	PRT;	770 AA.	
AC	P40763: O14916; Q9BW54;				O93598 brachydanio
DT	01-FEB-1995 (Rel. 31, Created)				Q6p943 brachydanio
DT	05-JUN-2004 (Rel. 44, Last sequence update)				P42228 mus musculus
DT	25-OCT-2004 (Rel. 45, Last annotation update)				Q14765 homo sapien
DE	Signal transducer and activator of transcription 3 (Acute-phase response factor).				Q66hb2 rattus norv
GN	Name=STAT3; Synonyms=APRF;				Q7zz77 brachydanio
OS	Homo sapiens (Human)				Q8aw24 brachydanio
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				Q8aw20 brachydanio
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				Q8aw24 brachydanio
OX	NCBI_TaxID=9606;				Q8aw24 brachydanio
LN	[1]				Q8aw24 brachydanio
RP	SEQUENCE FROM N.A. (ISOFORM 1).				Q8aw24 brachydanio
RC	TISSUE=Placenta;				Q8aw24 brachydanio
RX	MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;				Q8aw24 brachydanio
RA	Yoshida K., Sudo T., Naruto M., Kishimoto T.;				Q8aw24 brachydanio
RT	"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling pathway."				Q8aw24 brachydanio
RL	Cell 77:63-71 (1994).				Q8aw24 brachydanio
RN	[2]				Q8aw24 brachydanio
RP	SEQUENCE FROM N.A. (ISOFORM 1).				Q8aw24 brachydanio
RX	MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;				Q8aw24 brachydanio
RA	Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;				Q8aw24 brachydanio
RT	"Highly conserved amino-acid sequence between murine STAT3 and a revised human STAT3 sequence."				Q8aw24 brachydanio
RL	Gene 213:119-124 (1998).				Q8aw24 brachydanio
RN	[3]				Q8aw24 brachydanio
RP	SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT IL8-143.				Q8aw24 brachydanio
RA	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,				Q8aw24 brachydanio
RA	Rajkumar N., Yi Q., Nickerson D.A.;				Q8aw24 brachydanio
RT	"SeattlesNPs. NHLBI HUG6682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";				Q8aw24 brachydanio
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.				Q8aw24 brachydanio
RN	[4]				Q8aw24 brachydanio
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).				Q8aw24 brachydanio
RC	TISSUE=Kidney, and Pancreas;				Q8aw24 brachydanio
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				Q8aw24 brachydanio
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				Q8aw24 brachydanio
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				Q8aw24 brachydanio
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				Q8aw24 brachydanio
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				Q8aw24 brachydanio
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				Q8aw24 brachydanio
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,				Q8aw24 brachydanio
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				Q8aw24 brachydanio
RA	Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.H.,				Q8aw24 brachydanio
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				Q8aw24 brachydanio
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				Q8aw24 brachydanio
RA	Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				Q8aw24 brachydanio
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,				Q8aw24 brachydanio

ALIGNMENTS

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN SEQUENCE OF 564-704 FROM N.A.
RP TISSUE=Liver;
RC Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.,
RA Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
[6]
RN PHOSPHORYLATION ON SERINE.
RX MEDLINE=95215843; Pubmed=7701321;
RA Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.,
RT "Requirement of serine phosphorylation for formation of STAT-promoter
complexes.",
RL Science 267:1990-1994(1995).
[7]
RN INTERACTION WITH NCOAL.
RX Pubmed=11773079; DOI=10.1074/jbc.M11486200;
RA Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.,
RT "Functional interaction of STAT3 transcription factor with the
coactivator NcoA/SRC1a.",
RL J. Biol. Chem. 277:8004-8011(2002).
CC -I- FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6)-responsive elements identified in the promoters of various
acute-phase protein genes.
CC -I- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -I- SUBUNIT: Forms a homodimer or a heterodimer with a related family
member (at least STAT1). Interacts with NCOAL.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
in response to phosphorylation.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P40763-1; Sequence=Displayed;
CC Name=Del-701;
CC IsoId=P40763-2; Sequence=VSP_010474;
CC -I- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
muscle, kidney and pancreas.
CC -I- PM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
is important for the formation of stable DNA-binding STAT3
homodimers and maximal transcriptional activity.
CC -I- SIMILARITY: Belongs to the transcription factor STAT family.
CC -I- SIMILARITY: Contains 1 SH2 domain.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L29277; AAA58374.1; -;
CC EMBL; AJ012463; CAAL0032.1; -;
CC EMBL; AY572796; AAS66986.1; -;
CC EMBL; BC000627; AAH00627.1; -;
CC EMBL; BC014482; AAH14482.1; -;
CC EMBL; AF029311; AAB84254.1; -;
CC PIR; A54444; A54444.
CC HSP: P42227; IBL1.
CC TRANSFAC; T01493; -;
CC Genew; HGNC:11364; STAT3.
CC H-invDB; HIX0013840; -;
CC MIM; 102582; -;
CC GO; GO:0005737; Cytoplasm; TAS.
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. . .; TAS.

DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
DR GO; GO:0000122; P:negative regulation of transcription from P. . .; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS0001; SH2; 1.
KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
KW Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
FT VARSPLIC 701 701 Missing (in isoform Del-701).
FT VARIANT 32 32 Q -> K (in dbSNP:1803125).
FT VARIANT 143 143 M -> I.
FT CONFLICT 288 288 /FTID=VAR_018679.
FT CONFLICT 460 460 Q -> H (in Ref. 1).
FT CONFLICT 548 548 P -> S (in Ref. 1).
FT CONFLICT 561 561 K -> N (in Ref. 1).
FT CONFLICT 667 667 F -> Y (in Ref. 1).
FT CONFLICT 730 730 V -> L (in Ref. 1).
FT CONFLICT 770 770 T -> A (in Ref. 1).
SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
Query Match 99.0%; Score 792; DB 1; Length 770;
Best Local Similarity 98.7%; Pred. No. 7 3e-60;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQWNLQQLDTRYLKHLYSDTTPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
DB 1 MAQWNLQQLDTRYLKHLYSDTTPMELRQFLAPWIESQDWAYAASKESHATLVPHNL 60
QY 61 LGSDIQSYRFLQESNVLYOHNLRIKQFLOSYLEKPMELRIARIVARCLWEESRLQTAA 120
DB 61 LGSDIQSYRFLQESNVLYOHNLRIKQFLOSYLEKPMELRIARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQGANHPAAVVTKEQKQMLEQHLQDVRRK 154
DB 121 TAAQGGQGANHPAAVVTKEQKQMLEQHLQDVRRK 154
RESULT 2
STA3_MOUSE
ID STA3_MOUSE STANDARD; PRT; 770 AA.
AC P42227;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
response factor).
DE Name=Stat3; Synonyms=Aprf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
RP AND 632-640.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=94208062; Pubmed=7512451; DOI=10.1016/0092-8674(94)90235-6;
RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.,
RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
related transcription factor involved in the gp130-mediated signaling

RT pathway.";
RL Cell 77:63-71(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RX TISSUE=Thymus;
RA MEDLINE=94188718; PubMed=8140422;
RZ Zhong Z., Wen Z., Darnell J.E. Jr.;
RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
RL response to epidermal growth factor and interleukin-6.";
RL Science 264:95-98(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RX TISSUE=Brain;
RA MEDLINE=95014185; PubMed=7523373;
RZ Raz R., Durbin J.E., Levy D.E.;
RT "Acute phase response factor and additional members of the interferon-
RL stimulated gene factor 3 family integrate diverse signals from
RT cytokines, interferons, and growth factors.";
RL J. Biol. Chem. 269:24391-24395(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM STAT3B).
RX STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
RA MEDLINE=96016116; PubMed=7568080;
RZ Schaefer T.S., Sanders L.K., Nathans D.;
RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
RL form of Stat3.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RX STRAIN=129/SVJ;
RA PubMed=11161808; DOI=10.1006/geno.2000.6433;
RZ Miyoshi K., Cui Y., Riedlinger G., Lehoczy J., Zon L., Oka T.,
RA Dewar K., Hennighausen L.;
RT "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
RL zebrafish to mouse.";
RL Genomics 71:150-155(2001).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RX STRAIN=C57BL/6J, and NOD/LtJ;
RA Davoudi-Semimomi A., She J.-X.;
RT "A mutant Stat5b with weaker DNA binding defines a key defective
RL pathway in non-obese diabetic (NOD) mice.";
RL Submitted (MAY-2003) to the ENBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RX STRAIN=FVB/N; TISSUE=Mammary gland;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RZ Klausner R.L., Feingold E.A., Grouse L.H., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Iaquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.
RX MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
RZ Wen Z., Zhong Z., Darnell J.E. Jr.;
RT "Maximal activation of transcription by Stat1 and Stat3 requires both
RT tyrosine and serine phosphorylation."

RL Cell 82:241-250(1995).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
RX MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
RZ Becker S., Groner B., Mueller C.W.;
RT "Three-dimensional structure of the Stat3beta homodimer bound to
RN DNA.";
RL Nature 394:145-151(1998).
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes. STAT3B interacts with the N-terminal
CC part of JUN to activate such promoters in a cooperative way.
CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Stat3A;
CC IsoId=P42227-1; Sequence=Displayed;
CC Name=Stat3B;
CC IsoId=P42227-2; Sequence=VSP_006287;
CC Name=Del-701;
CC IsoId=P42227-3; Sequence=VSP_010475;
CC -!- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
CC kidney. STAT3B is also detected in the liver, although in a much
CC less abundant manner.
CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC -----
DR EMBL; L29278; AAA37254.1; -;
DR EMBL; U06922; AAA19452.1; -;
DR EMBL; U08378; AAA56668.1; -;
DR EMBL; U07079; AAC52612.1; -;
DR EMBL; AF246978; AAL59017.1; -;
DR EMBL; AY299489; AAQ75418.1; -;
DR EMBL; AY299490; AAQ75419.1; -;
DR EMBL; BC003806; AAH03806.1; -;
DR PIR; I49508; I49508.
DR PDB; 1BG1; X-ray; A=1-722.
DR TRANSFAC; T01574; -;
DR MGD; MGI:103038; Stat3.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0003677; F:DNA binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016563; F:transcriptional activator activity; IDA.
DR GO; GO:0007259; P:JAK-STAT cascade; IDA.
DR GO; GO:0006357; P:regulation of transcription from Pol II pro. .; IDA.
DR InterPro; IPR008967; P53 like DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
KW 3D-structure; Activator; Acute phase; Alternative splicing;
KW Direct protein sequencing; DNA-binding; Nuclear protein;

Phosphorylation; SH2 domain; Transcription regulation.
 KW DOMAIN 580 670 SH2.
 FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 FT MOD_RES 727 727 Phosphoserine.
 FT VARSPLIC 716 770 TTCSNTIDLPMSPTRLDLSLMQFGNGEGAPSPAGGQFESLT
 FT FDMDLTSECATSPM -> FIDAVWK (in isoform
 FT Stat3B).
 FT /FTid=VSP_006287.
 FT Missing (in isoform Del-701).
 FT /FTid=VSP_010475.
 FT S-A: Decreased transcriptional
 FT activation.
 FT MUTAGEN 727 727 E -> K (in Ref. 2).
 FT S -> T (in Ref. 2 and 4).
 FT M -> I (in Ref. 1).
 FT
 FT VARSPLIC 701 701
 FT
 FT MUTAGEN 727 727
 FT
 FT CONFLICT 16 16
 FT CONFLICT 25 25
 FT CONFLICT 394 394
 FT HELIX 139 180
 FT TURN 181 182
 FT TURN 197 198
 FT HELIX 199 237
 FT TURN 238 238
 FT HELIX 239 251
 FT TURN 252 253
 FT HELIX 261 290
 FT TURN 294 295
 FT TURN 297 301
 FT HELIX 302 320
 FT STRAND 321 328
 FT TURN 330 331
 FT TURN 333 334
 FT TURN 336 337
 FT STRAND 338 340
 FT TURN 341 342
 FT STRAND 345 351

Query Match 99.0%; Score 792; DB 1; Length 770;
 Best Local Similarity 98.7%; Pred. No. 7.3e-60;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHN 60
 DB 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHN 60
 QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLQATA 120
 DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLQATA 120
 QY 121 TAAQCGQGANHPHTAAVVTEKQQLMQLQDLQVRKR 154
 DB 121 TAAQCGQGANHPHTAAVVTEKQQLMQLQDLQVRKR 154

RESULT 3
 ID_STA3_RAT STANDARD; PRT; 770 AA.
 AC P52631;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3.
 GN Name=Stat3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.23998;
 RA Ripberger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,
 RA Fey G.H.;
 RT "Transcription factors Stat3 and Stat5b are present in rat liver
 RT nuclei late in an acute phase response and bind interleukin-6 response
 RT elements.";

J. Biol. Chem. 270:29998-30006(1995).
 RL -I- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes.
 CC -I- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -I- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL1 (By similarity).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation (By similarity).
 CC -I- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity (By similarity).
 CC -I- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -I- SIMILARITY: Contains 1 SH2 domain.
 CC
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 CC
 CC EMBL; X91810; CAAG2920.1; -
 CC DR HSSP; P42227; 1BG1.
 CC DR RGD; 3772; Stat3.
 CC DR InterPro; IPR008967; P53_like_DNA_bnd.
 CC DR InterPro; IPR009980; SH2.
 CC DR InterPro; IPR001217; STAT.
 CC DR Pfam; PF00017; SH2; 1.
 CC DR Pfam; PF01017; STAT_alpha; 1.
 CC DR Pfam; PF02864; STAT_bind; 1.
 CC DR Pfam; PF02865; STAT_int; 1.
 CC DR SMART; SM00252; SH2; 1.
 CC DR PROSITE; PS00001; SH2; 1.
 CC KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
 CC Transcription regulation.
 CC FT DOMAIN 580 670 SH2.
 CC FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 CC FT MOD_RES 727 727 Phosphoserine (By similarity).
 CC SQ SEQUENCE 770 AA; 88039 MW; D74A0C76954754ED CRC64;
 Query Match 99.0%; Score 792; DB 1; Length 770;
 Best Local Similarity 98.7%; Pred. No. 7.3e-60;
 Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHN 60
 DB 1 MAQWNQLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHN 60
 QY 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLQATA 120
 DB 61 LGEIDQOYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMELRIARIVARCLWEESRLQATA 120
 QY 121 TAAQCGQGANHPHTAAVVTEKQQLMQLQDLQVRKR 154
 DB 121 TAAQCGQGANHPHTAAVVTEKQQLMQLQDLQVRKR 154

RESULT 4
 ID_STA3_BOVIN STANDARD; PRT; 770 AA.
 AC P61635;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3.
 GN Name=STAT3;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.

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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
RT "The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus
RL during ruminant evolution.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes (By similarity).
CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation (By similarity).
CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ620655; CAF06182.1; -.
DR PROSITE; PS00001; SH2; 1.
KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
KW Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD RES 727 727 Phosphoserine (By similarity).
SQ SEQUENCE 770 AA; 87974 MW; 9CEB147C73E83274 CRC64;

Query Match 98.2%; Score 786; DB 1; Length 770;
Best Local Similarity 98.1%; Pred. No. 2.4e-59;
Matches 151; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
DB 1 MAQWNLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60

QY 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
DB 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

QY 121 TAAQGGQANHPTAAVTEKQOMLEQHLQDVYRKR 154
DB 121 TAAQGGQANHPTAAVTEKQOMLEQHLQDVYRKR 154

RESULT 5
Q6DV79 ID Q6DV79 PRELIMINARY; PRT; 771 AA.
AC DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Signal transducer and activator of transcription 3.
OS Gallus gallus (Chicken).
OC Archosauria; Aves; Neognathae; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Gallus.
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC Zhou G.Y., Leung F.C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641397; AAT64887.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.

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DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS00001; SH2; 1.
SQ SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;

Query Match 97.4%; Score 779; DB 2; Length 771;
Best Local Similarity 96.8%; Pred. No. 9.7e-59;
Matches 149; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
DB 1 MAQWNLQQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60

QY 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120
DB 61 LGEIDQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMETARIVARCLWEESRLQTAA 120

QY 121 TAAQGGQANHPTAAVTEKQOMLEQHLQDVYRKR 154
DB 121 TAAQGGQANHPTAAVTEKQOMLEQHLQDVYRKR 154

RESULT 6
Q9PVX8 ID Q9PVX8 PRELIMINARY; PRT; 769 AA.
AC DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat 3.
GN Name-stat 3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
RA Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
RA Asashima M., Yokota T.;
RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
RT embryos independent of BMP-4.";
RL Dev. Biol. 216:481-490(1999).
DR EMBL; AB017701; BAA86061.1; -.
DR HSSP; P42227; IBGL.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SMO0252; SH2; 1.
DR PROSITE; PS00001; SH2; 1.
SQ SEQUENCE 769 AA; 87974 MW; 0905C03263303069 CRC64;

Query Match 95.0%; Score 760; DB 2; Length 769;
Best Local Similarity 94.2%; Pred. No. 4.2e-57;
Matches 145; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNLQQLDTRYLEQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVPHNL 60
QY 61 LGEIDQYSRFLQESNVLYOHNLRRRIKQFLQSYLKPMEIARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQESNVLYOHNLRRRIKQFLQSYLKPMEIARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQGANHPAAVTEKQMLQHLQDVRKK 154
Db 121 TAAQGGQGANHPAAVTEKQMLQHLQDVRKK 154

RESULT 7
Q7ZXK3 PRELIMINARY; PRT; 766 AA.
ID Q7ZXK3
AC Q7ZXK3
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Stat3-A protein.
GN Name-stat3-A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044717; AHA44717.1; -.
DR HSSP; P42227; IBG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

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DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;

Query Match 93.6%; Score 749; DB 2; Length 766;
Best Local Similarity 92.2%; Pred. No. 3.7e-56;
Matches 142; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVPHNL 60
Db 1 MAQWNLQQLDTRYLEQLHQLYSDFPMLRQFLAPWIESQDWAYAASKESHATLVPHNL 60
QY 61 LGEIDQYSRFLQESNVLYOHNLRRRIKQFLQSYLKPMEIARIVARCLWEESRLQTAA 120
Db 61 LGEIDQYSRFLQESNVLYOHNLRRRIKQFLQSYLKPMEIARIVARCLWEESRLQTAA 120
QY 121 TAAQGGQGANHPAAVTEKQMLQHLQDVRKK 154
Db 121 TAAQGGQGANHPAAVTEKQMLQHLQDVRKK 154

RESULT 8
Q7ZTS5 PRELIMINARY; PRT; 414 AA.
ID Q7ZTS5
AC Q7ZTS5
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Stat3 protein.
GN Name-stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045276; AAH45276.1; -.
DR HSSP; P42227; IBG1.

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DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 414 AA; 49253 MW; 0FFD1B509B7526BD CRC64;

Query Match 86.8%; Score 694.5; DB 2; Length 414;
Best Local Similarity 86.4%; Pred. No. 9.3e-52;
Matches 133; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
Db 1 MAQWNLQQLDTRYLEQLYHLYSDSPFMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQENNVLYQHNLRIKQHLQSKYLEKPMELRIARVARCLWEESRLQT-A 119
QY 121 TAAQGGQGANHTAAVTEKQMLEQHLQDVRKR 154
Db 120 TTAQDQGVAAHTGTVTTEKQMLEHNLQDIRKR 153

RESULT 9
Q6NV46 PRELIMINARY; PRT; 786 AA.
ID Q6NV46
AC Q6NV46
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Stat3 protein.
GN Names=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RA Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC068320; AAH68320.1; -.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 786 AA; 90039 MW; FC7371D0B0E5447E CRC64;

Query Match 86.8%; Score 694.5; DB 2; Length 786;
Best Local Similarity 86.4%; Pred. No. 2e-51;
Matches 133; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
Db 1 MAQWNLQQLDTRYLEQLYHLYSDSPFMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELRIARVARCLWEESRLQTAA 120
Db 61 LGEIDQOYSRFLQENNVLYQHNLRIKQHLQSKYLEKPMELRIARVARCLWEESRLQT-A 119
QY 121 TAAQGGQGANHTAAVTEKQMLEQHLQDVRKR 154
Db 120 TTAQDQGVAAHTGTVTTEKQMLEHNLQDIRKR 153

RESULT 10
O93599 PRELIMINARY; PRT; 806 AA.
ID O93599
AC O93599;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor.
GN Names=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oates A.C.;
RL Thesis (1998), University of Melbourne, Australia.
DR EMBL; AJ005593; CAA06677.1; -.
DR HSSP; P42227; IBGI.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;

Query Match 86.8%; Score 694.5; DB 2; Length 806;
Best Local Similarity 86.4%; Pred. No. 2e-51;
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DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 785 AA; 89643 MW; 81F231BDE27DE938 CRC64;

Query Match      85.7%; Score 685.5; DB 2; Length 785;
Best Local Similarity 85.1%; Pred. No. 1.2e-50;
Matches 132; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

Qy 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MAQWNLQQLDTRYLEQLYHLYSDSPFMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LGEIDQOYSRFLQESNVLYQHNLRIKQHLQSKYLEKPMETARIVARCLWEESRLLOT-A 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 TAAQGGGOANHPTAAVVTKEQOMLEQHLQDVQRK 154
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 TSTSDQGSAAHPTGVVTEKQOILEHNLQDIDRK 153
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE STAT3
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Liu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -.
DR HSP; P42227; IBL1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FFE18BEFD8BE CRC64;

Query Match      85.2%; Score 681.5; DB 2; Length 764;
Best Local Similarity 85.7%; Pred. No. 2.5e-50;
Matches 132; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
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Db 1 MAQWNLQQLDTRYLEQLYHLYSDSPFMELRQFLAPWIESQDWAYAAKESHATLVSHNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LGEIDQOYSRFLQESNVLYQHNLRIKQHLQSKYLEKPMETARIVARCLWEESRLLOTAS 120
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Qy 121 TAAQGGGOANHPTAAVVTKEQOMLEQHLQDVQRK 154
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Db 121 TVAQD-GGAANPSTGVVTEKQOMLELNLQDIDRK 153
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RESULT 15

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Q8JGNO PRELIMINARY; PRT; 751 AA.
AC Q8JGNO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Statl.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21098508; PubMed=1164887; DOI=10.1016/S0145-305X(00)00050-1;
RA Turpen J.B., Carlson D.L., Huang C.;
RT "Cloning and developmental expression of Xenopus Statl.";
RL Dev. Comp. Immunol. 25:219-229(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Turpen J.B., Carlson D.L., Huang C.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101602; AAM51552.1; -.
DR HSP; P42224; IBL5.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR01217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 751 AA; 86497 MW; 788810A08B0889EA CRC64;

Query Match      50.1%; Score 401; DB 2; Length 751;
Best Local Similarity 48.7%; Pred. No. 4e-26;
Matches 75; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

Qy 1 MAQWNLQQLDTRYLKQHLQYSDTFPMELRQFLAPWIESQDWAYAAKESHATLVFHNL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MAQWYDLQQIDTKELEQVHQLYDSDSPFMELRQFLAPWLEQDWEHAANNYSVATILFHGL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMETARIVARCLWEESRLLOTAA 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LSQLDQOYSRFLQESNVLYQHNLRIKSKRNQLQDHFQEDPVQVAMINNCLESKILCNA- 119
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Qy 121 TAAQGGGOANHPTAAVVTKEQOMLEQHLQDVQRK 154
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 -RASNNQVSGSTQTTVMDKQKELDKKVDVRNR 152
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Search completed: May 5, 2005, 14:57:40
Job time : 43.6706 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 14:59:00 ; Search time 114.139 Seconds
(without alignments)
792.064 Million cell updates/sec

Title: US-10-090-185-9
Perfect score: 1388
Sequence: 1 RCLWESRLLOTATAAQQG.....LNVLKIKVICDKSDGVAA 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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19:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1388	100.0	271	13	US-10-090-185-9
2	1388	100.0	770	11	US-09-876-773-12
3	1388	100.0	770	17	US-10-639-617-12
4	1377	99.2	720	15	US-10-380-020-4
5	1377	99.2	769	15	US-10-380-020-2
6	1377	99.2	769	15	US-10-380-020-5
7	1377	99.2	770	14	US-10-045-792-8
8	1377	99.2	770	14	US-10-038-010-56
9	1377	99.2	770	14	US-10-117-087-2
10	1377	99.2	793	9	US-09-925-302-780
11	1377	99.2	793	10	US-09-925-302-780
12	1374	99.0	770	15	US-10-116-275-329
13	1372	98.8	770	15	US-10-116-275-349

14	1290	92.9	252	13	US-10-090-185-14	Sequence 14, Appl
15	1212	87.3	236	13	US-10-090-185-15	Sequence 15, Appl
16	1172	84.4	229	13	US-10-090-185-18	Sequence 18, Appl
17	1172	84.4	229	13	US-10-090-185-28	Sequence 28, Appl
18	1168	84.1	229	13	US-10-090-185-31	Sequence 31, Appl
19	1167	84.1	229	13	US-10-090-185-30	Sequence 30, Appl
20	1155	83.2	229	13	US-10-090-185-29	Sequence 29, Appl
21	1142	82.3	223	13	US-10-090-185-22	Sequence 22, Appl
22	1094	78.8	213	13	US-10-090-185-19	Sequence 23, Appl
23	943	67.9	185	13	US-10-090-185-23	Sequence 16, Appl
24	899	64.8	176	13	US-10-090-185-16	Sequence 17, Appl
25	723	52.1	143	13	US-10-090-185-17	Sequence 24, Appl
26	669	48.2	129	13	US-10-090-185-24	Sequence 4, Appl
27	654	47.1	749	9	US-09-833-205-4	Sequence 20, Appl
28	653	47.0	128	13	US-10-090-185-20	Sequence 12, Appl
29	647	46.6	268	13	US-10-090-185-12	Sequence 6, Appl
30	647	46.6	712	11	US-09-876-773-6	Sequence 2, Appl
31	647	46.6	712	14	US-10-245-120-2	Sequence 6, Appl
32	647	46.6	712	17	US-10-639-617-6	Sequence 5, Appl
33	647	46.6	712	17	US-10-936-390-5	Sequence 2, Appl
34	647	46.6	750	9	US-09-833-205-2	Sequence 4, Appl
35	647	46.6	750	11	US-09-876-773-4	Sequence 1, Appl
36	647	46.6	750	14	US-10-245-120-1	Sequence 44, Appl
37	647	46.6	750	14	US-10-308-279-44	Sequence 352, App
38	647	46.6	750	16	US-10-755-889-352	Sequence 823, App
39	647	46.6	750	16	US-10-755-889-823	Sequence 19, Appl
40	647	46.6	750	17	US-10-492-043-19	Sequence 4, Appl
41	647	46.6	750	17	US-10-639-617-4	Sequence 550, App
42	647	46.6	786	9	US-09-925-297-550	Sequence 3, Appl
43	623	44.9	582	14	US-10-245-120-3	Sequence 6, Appl
44	619	44.6	749	9	US-09-833-205-6	Sequence 8, Appl
45	619	44.6	749	11	US-09-876-773-8	

ALIGNMENTS

RESULT 1

US-10-090-185-9
; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR E
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-090-185-9

Query Match 100.0%; Score 1388; DB 13; Length 271;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	RCLWESRLLOTATAAQQGQGHHPHTAAVTEKQKMLEQHLQDVRRKRVQDLEQKMKVVE	60
Db	1	RCLWESRLLOTATAAQQGQGHHPHTAAVTEKQKMLEQHLQDVRRKRVQDLEQKMKVVE	60
Qy	61	NLQDDDFPNYKTLKSGQDMQDLGNNGSVTRQKMQLEQMLTALDQMRRSIVSELAGLLS	120
Db	61	NLQDDDFPNYKTLKSGQDMQDLGNNGSVTRQKMQLEQMLTALDQMRRSIVSELAGLLS	120

QY 121 AMEYVOKLTDEELADWKRPEIACIGGPNICLDRLNNWITSLAESQLOTRQOIKKLE 180
 Db 121 AMEYVOKLTDEELADWKRPEIACIGGPNICLDRLNNWITSLAESQLOTRQOIKKLE 180
 QY 181 LQOKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFT 240
 Db 181 LQOKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFT 240
 QY 241 TKVRLLVKFPPELNYQLKIKVICDKSGDVAA 271
 Db 241 TKVRLLVKFPPELNYQLKIKVICDKSGDVAA 271

RESULT 2
 US-09-876-773-12
 ; Sequence 12, Application US/09876773
 ; Publication No. US20040058318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; Fu, Xian-Yuan
 ; Wen, Zilong
 ; Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/876,773
 FILING DATE: 07-Jun-2001
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/212,185
 FILING DATE: 11-MAR-1994
 APPLICATION NUMBER: US 07/980,498
 FILING DATE: 23-NOV-1992
 APPLICATION NUMBER: US 07/854,296
 FILING DATE: 19-MAR-1992
 APPLICATION NUMBER: WO US93/02569
 FILING DATE: 19-MAR-1993
 APPLICATION NUMBER: US 08/126,588
 FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521

INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 770 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 12:
 US-09-876-773-12

Query Match 100.08; Score 1388; DB 11; Length 770;
 Best Local Similarity 100.08; Pred. No. 1e-109;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCLWEESRLLOTAATAAQGGQANHTAAVTEKQOMLEQHLQDVYKRVQDLEQKMKVVE 60
 Db 107 RCLWEESRLLOTAATAAQGGQANHTAAVTEKQOMLEQHLQDVYKRVQDLEQKMKVVE 166
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 Db 167 NLQDDPFDNFYKTLKSGQMDLNGNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLS 226
 QY 121 AMEYVOKLTDEELADWKRPEIACIGGPNICLDRLNNWITSLAESQLOTRQOIKKLE 180
 Db 227 AMEYVOKLTDEELADWKRPEIACIGGPNICLDRLNNWITSLAESQLOTRQOIKKLE 286
 QY 181 LQOKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFT 240
 Db 287 LQOKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFT 346
 QY 241 TKVRLLVKFPPELNYQLKIKVICDKSGDVAA 271
 Db 347 TKVRLLVKFPPELNYQLKIKVICDKSGDVAA 377

RESULT 3
 US-10-639-617-12
 ; Sequence 12, Application US/10639617
 ; Publication No. US20050079543A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; Fu, Xian-Yuan
 ; Wen, Zilong
 ; Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/639,617
 FILING DATE: 12-Aug-2003
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/212,185
 FILING DATE: 11-MAR-1994
 APPLICATION NUMBER: US 07/980,498
 FILING DATE: 23-NOV-1992
 APPLICATION NUMBER: US 07/854,296
 FILING DATE: 19-MAR-1992
 APPLICATION NUMBER: WO US93/02569
 FILING DATE: 19-MAR-1993
 APPLICATION NUMBER: US 08/126,588
 FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 770 amino acids

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;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

Query Match      100.0%; Score 1388; DB 17; Length 770;
Best Local Similarity 100.0%; Pred. No. 1e-109;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLQTAATAAQCGQANHTAAVVTKEQMLEQHLQDVRRKRVODLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQCGQANHTAAVVTKEQMLEQHLQDVRRKRVODLEQMKVVE 166

Qy 61 NLQDDFDNFYKTLKSQGMODLNGNNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDFDNFYKTLKSQGMODLNGNNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 226

Qy 121 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNITSLAESQLOTROQIKLEE 180
Db 227 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNITSLAESQLOTROQIKLEE 286

Qy 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPDRPLVIKTVQFT 240
Db 287 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPDRPLVIKTVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 377

RESULT 4
US-10-380-020-4
; Sequence 4, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-4

Query Match      99.2%; Score 1377; DB 15; Length 769;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 107 RCLWEESRLQTAATAAQCGQANHTAAVVTKEQMLEQHLQDVRRKRVODLEQMKVVE 166

Qy 61 NLQDDFDNFYKTLKSQGMODLNGNNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDFDNFYKTLKSQGMODLNGNNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 226

Qy 121 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNITSLAESQLOTROQIKLEE 180
Db 227 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNITSLAESQLOTROQIKLEE 286

Qy 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPDRPLVIKTVQFT 240
Db 287 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPDRPLVIKTVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 377

RESULT 5
US-10-380-020-2
; Sequence 2, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 769
; TYPE: PRT<
; ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match      99.2%; Score 1377; DB 15; Length 769;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCLWEESRLQTAATAAQCGQANHTAAVVTKEQMLEQHLQDVRRKRVODLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQCGQANHTAAVVTKEQMLEQHLQDVRRKRVODLEQMKVVE 166

Qy 61 NLQDDFDNFYKTLKSQGMODLNGNNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 120
Db 167 NLQDDFDNFYKTLKSQGMODLNGNNSVTRQKMQQLEQMLTALDQRRSIVSELAGLLS 226

Qy 121 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNITSLAESQLOTROQIKLEE 180
Db 227 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNITSLAESQLOTROQIKLEE 286

Qy 181 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPDRPLVIKTVQFT 240
Db 287 LQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPDRPLVIKTVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKDSGDVAA 377

RESULT 6
US-10-380-020-5
; Sequence 5, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 769
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-5

Query Match      99.2%; Score 1377; DB 15; Length 769;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCLWEESRLLOTAATAAQQGGQANHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 60
DB 107 RCLWEESRLLOTAATAAQQGGQANHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 166
QY 61 NLQDDDFNYKTLKSGQMDLNGNNSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLS 120
DB 167 NLQDDDFNYKTLKSGQMDLNGNNSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLS 226
QY 121 AMEYVQKTLTDEBLADWKRRPEIACIGGPPNICLDRLNNWITSLAESQLQTRQOIKKLEE 180
DB 227 AMEYVQKTLTDEBLADWKRRPEIACIGGPPNICLDRLNNWITSLAESQLQTRQOIKKLEE 286
QY 181 LOOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
DB 287 LOOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 271
DB 347 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 7
US-10-045-792-8
; Sequence 8, Application US/10045792
; Publication No. US20030003563A1
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; Moarefi, Ismail
; Darnell, Jr., James E.
; Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,792
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5900
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8

Query Match      99.2%; Score 1377; DB 14; Length 770;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCLWEESRLLOTAATAAQQGGQANHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 60
DB 107 RCLWEESRLLOTAATAAQQGGQANHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 166
QY 61 NLQDDDFNYKTLKSGQMDLNGNNSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLS 120
DB 167 NLQDDDFNYKTLKSGQMDLNGNNSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLS 226
QY 121 AMEYVQKTLTDEBLADWKRRPEIACIGGPPNICLDRLNNWITSLAESQLQTRQOIKKLEE 180
DB 227 AMEYVQKTLTDEBLADWKRRPEIACIGGPPNICLDRLNNWITSLAESQLQTRQOIKKLEE 286
QY 181 LOOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
DB 287 LOOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 271
DB 347 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 8
US-10-038-010-56
; Sequence 56, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: STAT3 : Transcription factor
; LOCATION: (1)..(770)
; OTHER INFORMATION:
US-10-038-010-56

Query Match      99.2%; Score 1377; DB 14; Length 770;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCLWEESRLLOTAATAAQQGGQANHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 60
DB 107 RCLWEESRLLOTAATAAQQGGQANHTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVE 166
QY 61 NLQDDDFNYKTLKSGQMDLNGNNSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLS 120
DB 167 NLQDDDFNYKTLKSGQMDLNGNNSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLS 226
QY 121 AMEYVQKTLTDEBLADWKRRPEIACIGGPPNICLDRLNNWITSLAESQLQTRQOIKKLEE 180
DB 227 AMEYVQKTLTDEBLADWKRRPEIACIGGPPNICLDRLNNWITSLAESQLQTRQOIKKLEE 286
QY 181 LOOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
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Db 287 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVKTGVQFT 346
Qy 241 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 271
Db 347 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 377

RESULT 9
US-10-117-087-2
; Sequence 2, Application US/10117087
; Publication No. US20030166854A1
; GENERAL INFORMATION:
; APPLICANT: SERLUPI-CRESCENZI, Ottaviano
; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
; FILE REFERENCE: SERLUPI-2
; CURRENT APPLICATION NUMBER: US/10/117,087
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/526,542
; PRIOR FILING DATE: 2000-03-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Human
US-10-117-087-2

Query Match 99.2%; Score 1377; DB 14; Length 770;
Best Local Similarity 99.3%; Pred. No. 9.1e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQKQMLEQHLQDVVRKQVQDLEQKMKVVE 60
Db 107 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQKQMLEQHLQDVVRKQVQDLEQKMKVVE 166

Qy 61 NLQDDDFNYKTLKSGQDMODLNGNOSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
Db 167 NLQDDDFNYKTLKSGQDMODLNGNOSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 226

Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESOLOTRQOIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESOLOTRQOIKKLEE 286

Qy 181 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVKTGVQFT 240
Db 287 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVKTGVQFT 346

Qy 241 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 271
Db 347 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 377

RESULT 10
US-09-925-302-780
; Sequence 780, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match 99.2%; Score 1377; DB 9; Length 793;
Best Local Similarity 99.3%; Pred. No. 9.4e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQKQMLEQHLQDVVRKQVQDLEQKMKVVE 60
Db 130 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQKQMLEQHLQDVVRKQVQDLEQKMKVVE 189

Qy 61 NLQDDDFNYKTLKSGQDMODLNGNOSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
Db 190 NLQDDDFNYKTLKSGQDMODLNGNOSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 249

Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESOLOTRQOIKKLEE 180
Db 250 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESOLOTRQOIKKLEE 309

Qy 181 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVKTGVQFT 240
Db 310 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVKTGVQFT 369

Qy 241 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 271
Db 370 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 400

RESULT 11

US-09-925-302-780
; Sequence 780, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match 99.2%; Score 1377; DB 10; Length 793;
Best Local Similarity 99.3%; Pred. No. 9.4e-109;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQKQMLEQHLQDVVRKQVQDLEQKMKVVE 60
Db 130 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQKQMLEQHLQDVVRKQVQDLEQKMKVVE 189

Qy 61 NLQDDDFNYKTLKSGQDMODLNGNOSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
Db 190 NLQDDDFNYKTLKSGQDMODLNGNOSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 249

Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESOLOTRQOIKKLEE 180
Db 250 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNMTSLAESOLOTRQOIKKLEE 309

Qy 181 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVKTGVQFT 240
Db 310 LQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVKTGVQFT 369

Qy 241 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 271
Db 370 TKVRLVKFPPELNYQLKIKVCIDKSGDVA 400

RESULT 12
US-10-116-275-329
; Sequence 329, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 329
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Rat
US-10-116-275-329

Query Match 99.8%; Score 1374; DB 15; Length 770;
Best Local Similarity 98.9%; Pred. No. 1.6e-108;
Matches 268; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RCLWEESRLLOTAATAAQQGQANHPPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVE 60
Db 107 RCLWEESRLLOTAATAAQQGQANHPPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVE 166
Qy 61 NLQDDDFNYKTLKSQGMQDLNGNNSVTRQKMOQLEOMLTALDOMRSIVSELAGLLS 120
Db 167 NLQDDDFNYKTLKSQGMQDLNGNNSVTRQKMOQLEOMLTALDOMRSIVSELAGLLS 226
Qy 121 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWIITSLAESQLQTRQOIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWIITSLAESQLQTRQOIKKLEE 286
Qy 181 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
Db 287 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 13
US-10-116-275-349
; Sequence 349, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 349
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-116-275-349

Query Match 98.8%; Score 1372; DB 15; Length 770;
Best Local Similarity 98.9%; Pred. No. 2.4e-108;
Matches 268; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RCLWEESRLLOTAATAAQQGQANHPPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVE 60
Db 107 RCLWEESRLLOTAATAAQQGQANHPPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVE 166
Qy 61 NLQDDDFNYKTLKSQGMQDLNGNNSVTRQKMOQLEOMLTALDOMRSIVSELAGLLS 120
Db 167 NLQDDDFNYKTLKSQGMQDLNGNNSVTRQKMOQLEOMLTALDOMRSIVSELAGLLS 226
Qy 121 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWIITSLAESQLQTRQOIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWIITSLAESQLQTRQOIKKLEE 286
Qy 181 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
Db 287 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 14

US-10-090-185-14
; Sequence 14, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR PR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14

Query Match 92.9%; Score 1290; DB 13; Length 252;
Best Local Similarity 100.0%; Pred. No. 5.7e-102;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCLWEESRLLOTAATAAQQGQANHPPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVE 60
Db 1 RCLWEESRLLOTAATAAQQGQANHPPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVE 60
Qy 61 NLQDDDFNYKTLKSQGMQDLNGNNSVTRQKMOQLEOMLTALDOMRSIVSELAGLLS 120
Db 61 NLQDDDFNYKTLKSQGMQDLNGNNSVTRQKMOQLEOMLTALDOMRSIVSELAGLLS 120
Qy 121 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWIITSLAESQLQTRQOIKKLEE 180
Db 121 AMEYVQKTLTDEELADWKRPEIACIGPPNICLDRLNWIITSLAESQLQTRQOIKKLEE 180
Qy 181 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
Db 181 LQKVSYKGDPIVOHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
Qy 241 TKVRLLVKFPPEL 252

Db 241 TKVRLVKPEL 252

RESULT 15

US-10-090-185-15
 ; Sequence 15, Application US/10090185
 ; Publication No. US20020197647A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Xiaokui
 ; APPLICANT: Wzieszczyńska, Melissa H
 ; APPLICANT: Horvath, Curt M
 ; APPLICANT: Darnell Jr., James E
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR P
 ; TITLE OF INVENTION: INTERACTIONS
 ; FILE REFERENCE: 600-1-253
 ; CURRENT APPLICATION NUMBER: US/10/090,185
 ; CURRENT FILING DATE: 2002-03-04
 ; PRIOR APPLICATION NUMBER: 09/387,418
 ; PRIOR FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-090-185-15

Query Match 87.3%; Score 1212; DB 13; Length 236;
 Best Local Similarity 100.0%; Pred. No. 2.4e-95;
 Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RCLWEESRLLOTAATAAQCGQANHPTAAVVTETKQMLEQHLQDVVKRVQDLEQMKVVE 60
 Db 1 RCLWEESRLLOTAATAAQCGQANHPTAAVVTETKQMLEQHLQDVVKRVQDLEQMKVVE 60
 Qy 61 NLQDDDFNFKYTKLSQGMODLNGNOSVTRQKWOOLEOMLTALDQMRRSIVSELAGLS 120
 Db 61 NLQDDDFNFKYTKLSQGMODLNGNOSVTRQKWOOLEOMLTALDQMRRSIVSELAGLS 120
 Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 180
 Db 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 180
 Qy 181 LQKVSYKGDPIVQHRPMLERIIVELFRNLKMSAFVVERQCPMPHDPRLVIKGTG 236
 Db 181 LQKVSYKGDPIVQHRPMLERIIVELFRNLKMSAFVVERQCPMPHDPRLVIKGTG 236

Search completed: May 5, 2005, 15:17:41
 Job time : 115.139 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 14:55:35 ; Search time 40.8094 Seconds
(without alignments)
495.716 Million cell updates/sec

Title: US-10-090-185-9
Perfect score: 1388
Sequence: 1 RCLWESRLLOTAATAAQQG.....LNVQLKIKVICDKSDGVA 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1388	100.0	271	3	US-09-387-418A-9
2	1388	100.0	770	1	US-08-369-796-12
3	1388	100.0	770	2	US-08-852-091-12
4	1388	100.0	770	2	US-08-820-754-12
5	1388	100.0	770	3	US-08-956-652-12
6	1388	100.0	770	3	US-08-956-869-12
7	1388	100.0	770	3	US-08-948-547-12
8	1388	100.0	770	3	US-09-364-970-3
9	1388	100.0	770	3	US-09-364-970-5
10	1388	100.0	770	3	US-08-956-653A-12
11	1388	100.0	770	4	US-08-212-185-12
12	1388	100.0	770	5	PCT-US95-17025-12
13	1377	99.2	770	1	US-08-416-581B-9
14	1377	99.2	770	3	US-09-012-710-8
15	1377	99.2	770	3	US-09-556-273-8
16	1377	99.2	770	4	US-09-526-542-2
17	1377	99.2	770	4	US-10-117-087-2
18	1372	98.8	770	1	US-08-416-581B-1
19	1372	98.8	770	1	US-08-416-581B-5
20	1372	98.8	770	3	US-09-087-465-6
21	1372	98.8	770	4	US-09-972-800A-6
22	1372	98.8	771	1	US-08-276-099A-14
23	1372	98.8	771	1	US-08-781-890-14
24	1290	92.9	252	3	US-09-387-418A-14
25	1212	87.3	236	3	US-09-387-418A-15
26	1172	84.4	229	3	US-09-387-418A-18
27	1172	84.4	229	3	US-09-387-418A-28

28	1168	84.1	229	3	US-09-387-418A-31	Sequence 31, Appl
29	1167	84.1	229	3	US-09-387-418A-30	Sequence 30, Appl
30	1155	83.2	229	3	US-09-387-418A-29	Sequence 29, Appl
31	1142	82.3	223	3	US-09-387-418A-22	Sequence 22, Appl
32	1094	78.8	213	3	US-09-387-418A-19	Sequence 19, Appl
33	943	67.9	185	3	US-09-387-418A-23	Sequence 23, Appl
34	899	64.8	176	3	US-09-387-418A-16	Sequence 16, Appl
35	723	52.1	143	3	US-09-387-418A-17	Sequence 17, Appl
36	669	48.2	129	3	US-09-387-418A-24	Sequence 24, Appl
37	653	47.0	128	3	US-09-387-418A-20	Sequence 20, Appl
38	647	46.6	268	3	US-09-387-418A-12	Sequence 12, Appl
39	647	46.6	712	1	US-08-369-796-6	Sequence 6, Appl
40	647	46.6	712	2	US-08-852-091-6	Sequence 6, Appl
41	647	46.6	712	2	US-08-820-754-6	Sequence 6, Appl
42	647	46.6	712	3	US-08-956-652-6	Sequence 6, Appl
43	647	46.6	712	3	US-08-956-869-6	Sequence 6, Appl
44	647	46.6	712	3	US-08-948-547-6	Sequence 6, Appl
45	647	46.6	712	3	US-08-956-653A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-387-418A-9
; Sequence 9, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-9

Query Match	100.0%;	Score 1388;	DB 3;	Length 271;
Best Local Similarity	100.0%;	Pred. No. 4.2e-119;		
Matches	271;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	RCLWESRLLOTAATAAQQGQANHPPTAAVVTXKQOMLEOHLOQDVVRKRVODLEQMKVVE	60	
Db	1	RCLWESRLLOTAATAAQQGQANHPPTAAVVTXKQOMLEOHLOQDVVRKRVODLEQMKVVE	60	
Qy	61	NLODDFDNFYKTLKSGQMDLNGNQSOTRQKQOOLEOMLTALDQMRSTVSELAGLLS	120	
Db	61	NLODDFDNFYKTLKSGQMDLNGNQSOTRQKQOOLEOMLTALDQMRSTVSELAGLLS	120	
Qy	121	AMEYVQKTLDEELADWKRRPEIACIGPPNIICLDRLENNWITSLSAQLOTRQIQIKLEE	180	
Db	121	AMEYVQKTLDEELADWKRRPEIACIGPPNIICLDRLENNWITSLSAQLOTRQIQIKLEE	180	
Qy	181	LOQKVSYKGDPIVOHRPMLERIVEFRNLKMSAFVVERQPCMPHDPRLIVIKTGVQFT	240	
Db	181	LOQKVSYKGDPIVOHRPMLERIVEFRNLKMSAFVVERQPCMPHDPRLIVIKTGVQFT	240	
Qy	241	TKVRLLVKFFELNYQLKVICDKSDGVA 271		
Db	241	TKVRLLVKFFELNYQLKVICDKSDGVA 271		

RESULT 2
US-08-369-796-12
; Sequence 12, Application US/08369796

Patent No. 5716622
 GENERAL INFORMATION:
 APPLICANT: James E. Darnell, Jr.
 APPLICANT: Zilong Wen
 APPLICANT: Curt M. Horvath
 APPLICANT: Zhong Zhong
 TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
 TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/369,796
 FILING DATE: 06-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-116
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 770 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-369-796-12

Query Match 100.0%; Score 1388; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 1.7e-118;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCLWEESRLLOTAATAAQQGGQANHTAAVTEKQMLQHLQDVRRKRVQDLEQMKVVE 60
 DB 107 RCLWEESRLLOTAATAAQQGGQANHTAAVTEKQMLQHLQDVRRKRVQDLEQMKVVE 166
 QY 61 NLQDDFDNFYKTLKSGQMDLNGNNSQVTRQKMQLEQMLTALDQMRRSIVSELAGLLS 120
 DB 167 NLQDDFDNFYKTLKSGQMDLNGNNSQVTRQKMQLEQMLTALDQMRRSIVSELAGLLS 226
 QY 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLQTRQIKKLEE 180
 DB 227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLQTRQIKKLEE 286
 QY 181 LQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
 DB 287 LQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
 QY 241 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 271
 DB 347 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

RESULT 3
 US-08-852-091-12
 ; Sequence 12, Application US/08852091
 ; Patent No. 5883228
 ; GENERAL INFORMATION:
 ; APPLICANT: James E. Darnell, Jr.
 ; APPLICANT: Zilong Wen

APPLICANT: Curt M. Horvath
 APPLICANT: Zhong Zhong
 TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
 TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/852,091
 FILING DATE: 06-MAY-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/369,796
 FILING DATE: 06-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-116
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 770 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-852-091-12

Query Match 100.0%; Score 1388; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 1.7e-118;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCLWEESRLLOTAATAAQQGGQANHTAAVTEKQMLQHLQDVRRKRVQDLEQMKVVE 60
 DB 107 RCLWEESRLLOTAATAAQQGGQANHTAAVTEKQMLQHLQDVRRKRVQDLEQMKVVE 166
 QY 61 NLQDDFDNFYKTLKSGQMDLNGNNSQVTRQKMQLEQMLTALDQMRRSIVSELAGLLS 120
 DB 167 NLQDDFDNFYKTLKSGQMDLNGNNSQVTRQKMQLEQMLTALDQMRRSIVSELAGLLS 226
 QY 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLQTRQIKKLEE 180
 DB 227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLQTRQIKKLEE 286
 QY 181 LQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
 DB 287 LQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
 QY 241 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 271
 DB 347 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

RESULT 4
 US-08-820-754-12
 ; Sequence 12, Application US/08820754
 ; Patent No. 5976835
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan

APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-820-754-12

Query Match 100.0%; Score 1388; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCLWEESRLQTAATAAQGGQANHTAAVTEKQMLEQHLQDVVRKVQDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHTAAVTEKQMLEQHLQDVVRKVQDLEQMKVVE 166
Qy 61 NLQDDDFPNYKTLKSGQMDLNGNOSVTRQKMOLEOMLTALDQMRRSIVSELGLLS 120
Db 167 NLQDDDFPNYKTLKSGQMDLNGNOSVTRQKMOLEOMLTALDQMRRSIVSELGLLS 226
Qy 121 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTTSIAESQLOTRQIQKLEE 180
Db 227 AMEVVQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTTSIAESQLOTRQIQKLEE 286
Qy 181 LQQKSVYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPHDPRLIVKTVQFT 240
Db 287 LQQKSVYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPHDPRLIVKTVQFT 346
Qy 241 TKVRLLVKFPPELVQLKIKVICIDKSGDVAA 271
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Db 347 TKVRLLVKFPPELVQLKIKVICIDKSGDVAA 377
RESULT 5
US-08-956-652-12
Sequence 12, Application US/08956652
Patent No. 6013475
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-956-652-12

Query Match 100.0%; Score 1388; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCLWEESRLQTAATAAQGGQANHTAAVTEKQMLEQHLQDVVRKVQDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHTAAVTEKQMLEQHLQDVVRKVQDLEQMKVVE 166
Qy 61 NLQDDDFPNYKTLKSGQMDLNGNOSVTRQKMOLEOMLTALDQMRRSIVSELGLLS 120
Db 167 NLQDDDFPNYKTLKSGQMDLNGNOSVTRQKMOLEOMLTALDQMRRSIVSELGLLS 226

QY 121 AMEYVQKTLTDEELADWKRPETACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 180
 Db 227 AMEYVQKTLTDEELADWKRPETACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 286
 QY 181 LQOKSVYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFT 240
 Db 287 LQOKSVYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFT 346
 QY 241 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 271
 Db 347 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 377

RESULT 6
 US-08-956-869-12
 ; Sequence 12, Application US/08956869
 ; Patent No. 6030808
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan
 ; APPLICANT: Wen, Zilong
 ; APPLICANT: Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/956,869
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/212,185
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/854,296
 ; FILING DATE: 19-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO US93/02569
 ; FILING DATE: 19-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/126,588
 ; FILING DATE: 24-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-956-869-12

Query Match 100.08; Score 1388; DB 3; Length 770;
 Best Local Similarity 100.08; Pred. No. 1.7e-118;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCLWESRLLOTAATAAQOGGOANHPATAAVTEKQOMLEQHLQDVKRKRVQDLEQKMKVYE 60
 Db 107 RCLWESRLLOTAATAAQOGGOANHPATAAVTEKQOMLEQHLQDVKRKRVQDLEQKMKVYE 166
 QY 61 NLQDDPDFNYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 120
 Db 167 NLQDDPDFNYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLS 226
 QY 121 AMEYVQKTLTDEELADWKRPETACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 180
 Db 227 AMEYVQKTLTDEELADWKRPETACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 286
 QY 181 LQOKSVYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFT 240
 Db 287 LQOKSVYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFT 346
 QY 241 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 271
 Db 347 TKVRLLVKFPPELNYQLKIKVICIDKSGDVAA 377

RESULT 7
 US-08-948-547-12
 ; Sequence 12, Application US/08948547
 ; Patent No. 6124118
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan
 ; APPLICANT: Wen, Zilong
 ; APPLICANT: Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/948,547
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/212,185
 ; FILING DATE: 11-MAR-1994
 ; APPLICATION NUMBER: US 07/980,498
 ; FILING DATE: 23-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/854,296
 ; FILING DATE: 19-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO US93/02569
 ; FILING DATE: 19-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/126,588
 ; FILING DATE: 24-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684


```
TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-948-547-12

Query Match      100.0%; Score 1388; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLQTAATAAQCGQANHPHTAAVVTKEQOMLEOHLDVRRKVDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQCGQANHPHTAAVVTKEQOMLEOHLDVRRKVDLEQMKVVE 166
Qy 61 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLS 120
Db 167 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLS 226
Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNMTSIAESQLQTRQIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNMTSIAESQLQTRQIKKLEE 286
Qy 181 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 240
Db 287 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 346
Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 8
US-09-364-970-3
; Sequence 3, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPLASIA/PROLIFERATIVE CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT APPLICATION NUMBER: US/09/364,970
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 3
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-3

Query Match      100.0%; Score 1388; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLQTAATAAQCGQANHPHTAAVVTKEQOMLEOHLDVRRKVDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQCGQANHPHTAAVVTKEQOMLEOHLDVRRKVDLEQMKVVE 166
Qy 61 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLS 120
Db 167 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLS 226
Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNMTSIAESQLQTRQIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNMTSIAESQLQTRQIKKLEE 286
Qy 181 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 240
Db 287 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 346

US-08-956-653A-12
; Sequence 12, Application US/0895653A
; Patent No. 6338949
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 9
US-09-364-970-5
; Sequence 5, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPLASIA/PROLIFERATIVE CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT APPLICATION NUMBER: US/09/364,970
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-5

Query Match      100.0%; Score 1388; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLQTAATAAQCGQANHPHTAAVVTKEQOMLEOHLDVRRKVDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQCGQANHPHTAAVVTKEQOMLEOHLDVRRKVDLEQMKVVE 166
Qy 61 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLS 120
Db 167 NLQDDDFNFKTLKSGQDMQDLNNGNSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLS 226
Qy 121 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNMTSIAESQLQTRQIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNMTSIAESQLQTRQIKKLEE 286
Qy 181 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 240
Db 287 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVKTGVQFT 346
Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 10
US-08-956-653A-12
; Sequence 12, Application US/0895653A
; Patent No. 6338949
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/956,653A
FILING DATE: 11-MAR-1994
CLASSIFICATION: US 08/212,185
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-956-653A-12

Query Match 100.0%; Score 1388; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCLWEESRLIQTAAATAAQGGQANHPPTAAVVTKEQOMLEOHLDQVRRKRVQDLQKMKVVE 60
Db 107 RCLWEESRLIQTAAATAAQGGQANHPPTAAVVTKEQOMLEOHLDQVRRKRVQDLQKMKVVE 166
Qy 61 NLQDDDFNYKTLKSGQMDLNGNNSVTRQKMQLEOMLTALDOMRRSIVSELAGLLS 120
Db 167 NLQDDDFNYKTLKSGQMDLNGNNSVTRQKMQLEOMLTALDOMRRSIVSELAGLLS 226
Qy 121 AMEVVQKTLTDEELADWKRPEIACIGPPNIICLDRLENWITSIAESQLOTRQOIKKLEE 180
Db 227 AMEVVQKTLTDEELADWKRPEIACIGPPNIICLDRLENWITSIAESQLOTRQOIKKLEE 286
Qy 181 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPRLVIKTGVQFT 240
Db 287 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPRLVIKTGVQFT 346
Qy 241 TKVRLLVKFPPELNYQLKIKVICIDKSDGVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKSDGVAA 377

RESULT 11
US-08-212-185-12
Sequence 12, Application US/08212185
Patent No. 6605442
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-212-185-12

Query Match 100.0%; Score 1388; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCLWEESRLIQTAAATAAQGGQANHPPTAAVVTKEQOMLEOHLDQVRRKRVQDLQKMKVVE 60
Db 107 RCLWEESRLIQTAAATAAQGGQANHPPTAAVVTKEQOMLEOHLDQVRRKRVQDLQKMKVVE 166
Qy 61 NLQDDDFNYKTLKSGQMDLNGNNSVTRQKMQLEOMLTALDOMRRSIVSELAGLLS 120
Db 167 NLQDDDFNYKTLKSGQMDLNGNNSVTRQKMQLEOMLTALDOMRRSIVSELAGLLS 226
Qy 121 AMEVVQKTLTDEELADWKRPEIACIGPPNIICLDRLENWITSIAESQLOTRQOIKKLEE 180
Db 227 AMEVVQKTLTDEELADWKRPEIACIGPPNIICLDRLENWITSIAESQLOTRQOIKKLEE 286
Qy 181 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPRLVIKTGVQFT 240
Db 287 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHDPRLVIKTGVQFT 346
Qy 241 TKVRLLVKFPPELNYQLKIKVICIDKSDGVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVICIDKSDGVAA 377

RESULT 12
PCT-US95-17025-12

; Sequence 12, Application PC/TUS9517025
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17025
; FILING DATE: 28-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-17025-12

Query Match 100.0%; Score 1388; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.7e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RCLWEESRLQTAATAAQGGQANHPHTAAVVTEKQQLQHLQDVVKRVQDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHPHTAAVVTEKQQLQHLQDVVKRVQDLEQMKVVE 166
Qy 61 NLQDDFDNFYKTLKSQGMQDLNNGNSVTRQKMQQLQHLQDVVKRVQDLEQMKVVE 120
Db 167 NLQDDFDNFYKTLKSQGMQDLNNGNSVTRQKMQQLQHLQDVVKRVQDLEQMKVVE 226
Qy 121 AMEVQKTLTDEELADWKRPETACIGPPNICLDRLNNWITSLSAQSLOTROQIKKLEE 180
Db 227 AMEVQKTLTDEELADWKRPETACIGPPNICLDRLNNWITSLSAQSLOTROQIKKLEE 286
Qy 181 LQKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFT 240
Db 287 LQKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFT 346

Qy 241 TKVRLVKFPPELNYQLKIKVCIDKDSGDVAA 271
Db 347 TKVRLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 13
US-08-416-581B-9
; Sequence 9, Application US/08416581B

; Patent No. 5719042
; GENERAL INFORMATION:
; APPLICANT: Kishimoto, Tadimitsu
; APPLICANT: Akira, Shizuo
; TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,581B
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-65825/1994
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: Q-37891
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-416-581B-9

Query Match 99.2%; Score 1377; DB 1; Length 770;
Best Local Similarity 99.3%; Pred. No. 1.7e-117;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RCLWEESRLQTAATAAQGGQANHPHTAAVVTEKQQLQHLQDVVKRVQDLEQMKVVE 60
Db 107 RCLWEESRLQTAATAAQGGQANHPHTAAVVTEKQQLQHLQDVVKRVQDLEQMKVVE 166
Qy 61 NLQDDFDNFYKTLKSQGMQDLNNGNSVTRQKMQQLQHLQDVVKRVQDLEQMKVVE 120
Db 167 NLQDDFDNFYKTLKSQGMQDLNNGNSVTRQKMQQLQHLQDVVKRVQDLEQMKVVE 226
Qy 121 AMEVQKTLTDEELADWKRPETACIGPPNICLDRLNNWITSLSAQSLOTROQIKKLEE 180
Db 227 AMEVQKTLTDEELADWKRPETACIGPPNICLDRLNNWITSLSAQSLOTROQIKKLEE 286
Qy 181 LQKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFT 240
Db 287 LQKVSYKGPPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFT 346

RESULT 14
US-09-012-710-8
; Sequence 8, Application US/09012710
; Patent No. 6087478
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moareffi, Ismail
; APPLICANT: Darnell, Jr., James E.

APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-012-710-8

Query Match 99.2%; Score 1377; DB 3; Length 770;
Best Local Similarity 99.3%; Pred. No. 1.7e-117;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RCLWEESRLLOTAATAAQGGQANHPPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVE 60
DB 107 RCLWEESRLLOTAATAAQGGQANHPPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVE 166
QY 61 NLODDDFNYKTLKSGQDMQDLNNGNQSVTQKMQOLEQMLTALDQMRRSIVSELAGLLS 120
DB 167 NLODDDFNYKTLKSGQDMQDLNNGNQSVTQKMQOLEQMLTALDQMRRSIVSELAGLLS 226
QY 121 AMEYVQKLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 180
DB 227 AMEYVQKLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 286
QY 181 LQOKVSYKGDPIVQHRPMLPEERIVELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFT 240
DB 287 LQOKVSYKGDPIVQHRPMLPEERIVELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 271
DB 347 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

RESULT 15

US-09-556-273-8

Sequence 8, Application US/09556273

Patent No. 6312887

GENERAL INFORMATION:

APPLICANT: Vinkemeier, Uwe

APPLICANT: Moarefi, Ismail

APPLICANT: Darnell, Jr., James E.

APPLICANT: Kuriyan, John

TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A

TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,273
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-556-273-8

Query Match 99.2%; Score 1377; DB 3; Length 770;
Best Local Similarity 99.3%; Pred. No. 1.7e-117;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RCLWEESRLLOTAATAAQGGQANHPPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVE 60
DB 107 RCLWEESRLLOTAATAAQGGQANHPPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVE 166
QY 61 NLODDDFNYKTLKSGQDMQDLNNGNQSVTQKMQOLEQMLTALDQMRRSIVSELAGLLS 120
DB 167 NLODDDFNYKTLKSGQDMQDLNNGNQSVTQKMQOLEQMLTALDQMRRSIVSELAGLLS 226
QY 121 AMEYVQKLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 180
DB 227 AMEYVQKLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 286
QY 181 LQOKVSYKGDPIVQHRPMLPEERIVELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFT 240
DB 287 LQOKVSYKGDPIVQHRPMLPEERIVELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFT 346
QY 241 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 271
DB 347 TKVRLLVKFPPELNYQLKIKVCIDKSDGVAA 377

Search completed: May 5, 2005, 14:58:52

Job time : 41.8094 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2005, 14:55:35 ; Search time 84.1694 Seconds
(without alignments)
1245.251 Million cell updates/sec

Title: US-10-090-185-9

Perfect score: 1388

Sequence: 1 RCLWESRLLOTATAAQQG.....LNVLKIKVCIDKSDGVAA 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1388	100.0	271	4	AAY72841 Mouse Sta
2	1388	100.0	770	2	AAR72082 Mouse Sta
3	1388	100.0	770	2	AAW03176 Mouse Sta
4	1377	99.2	720	5	AAE22055 Human Sta
5	1377	99.2	769	5	ABB57164 Mouse isc
6	1377	99.2	769	5	AAE22054 Human Sta
7	1377	99.2	769	5	AAE22056 Human pro
8	1377	99.2	770	2	AAR82995 Mouse liv
9	1377	99.2	770	2	AAY03768 Human STA
10	1377	99.2	770	3	AAH12377 N-termina
11	1377	99.2	770	5	AAE14652 Murine ST
12	1377	99.2	770	5	ABG69497 Human bai
13	1377	99.2	770	6	ABU10476 Mouse Sta
14	1377	99.2	770	8	ADN04365 Antipsori
15	1377	99.2	770	8	ADP54789 Human PRO
16	1377	99.2	793	3	AB58442 Lung canc
17	1374	99.0	770	7	ADD44738 Rat Prote
18	1372	98.8	770	2	AAR82993 Human pla
19	1372	98.8	770	4	AB119964 Human sig
20	1372	98.8	770	5	AAE15174 Human Sta
21	1372	98.8	770	7	ADD44740 Human pro
22	1290	92.9	252	4	AAY72846 Mouse Sta
23	1212	87.3	236	4	AAY72847 Mouse Sta
24	1172	84.4	229	4	AAY72850 Mouse Sta
25	1168	84.1	229	4	AAY72863 Mouse Sta

26	1167	84.1	229	4	AAY72862	Aay72862 Mouse Sta
27	1157.5	83.4	228	4	AAY72861	Aay72861 Mouse Sta
28	1146	82.6	229	4	AAY72860	Aay72860 Mouse Sta
29	1142	82.3	223	4	AAY72854	Aay72854 Mouse Sta
30	1094	78.8	213	4	AAY72851	Aay72851 Mouse Sta
31	943	67.9	185	4	AAY72855	Aay72855 Mouse Sta
32	899	64.8	176	4	AAY72848	Aay72848 Mouse Sta
33	723	52.1	143	4	AAY72849	Aay72849 Mouse Sta
34	669	48.2	129	4	AAY72856	Aay72856 Mouse Sta
35	654	47.1	749	5	AAG78526	Aag78526 Rat STAT-
36	653	47.0	128	4	AAY72852	Aay72852 Mouse Sta
37	647	46.6	268	4	AAY72844	Aay72844 Mouse Sta
38	647	46.6	680	6	ABR59713	AbR59713 Human sig
39	647	46.6	712	2	AAR72079	Aar72079 Human STA
40	647	46.6	712	2	AAW03170	Aaw03170 Human STA
41	647	46.6	712	2	AAW62995	Aaw62995 Human Sta
42	647	46.6	712	6	ABU04747	Abu04747 Human exp
43	647	46.6	712	6	ABU04735	Abu04735 Human exp
44	647	46.6	712	6	ABU04745	Abu04745 Human exp
45	647	46.6	712	6	ABU04743	Abu04743 Human exp

ALIGNMENTS

RESULT 1

AAY72841

ID AAY72841 standard; protein; 271 AA.

XX AAY72841;

XX 31-MAY-2001 (first entry)

XX Mouse Stat3 protein fragment #2 (107-377 amino acids).

XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;

KW cellular transformation; dysproliferative disease; cancer; psoriasis;

KW therapy.

XX Mus musculus.

XX Key

XX Region

XX Location/Qualifiers

XX 24..48

XX /note= "Stat3-c-Jun interaction region 1; corresponds to

130-154 position of Stat3 protein"

XX 236..252

XX /note= "Stat3-c-Jun interaction region 2; corresponds to

342-358 position of Stat3 protein"

XX WO200116605-A2.

XX 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US023822.

XX 31-AUG-1999; 99US-00387418.

XX (UVRQ) UNIV ROCKEFELLER.

XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;

XX WPI; 2001-226705/23.

XX Identifying an agent for use in modulating the interaction between

XX transcription factor c-Jun and a Stat3 protein.

XX Claim 65; Page 67-68; 86pp; English.

XX The present sequence is mouse Stat3 protein fragment containing 107-377

XX amino acids of Stat3 protein. This Stat3 fragment showed strong binding

XX to c-Jun protein in the cell extract. The invention relates to methods

XX for identifying interacting regions of transcription factors and methods

XX for identifying agents which modulates the interaction between a

CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 271 AA;

Query Match 100.0%; Score 1388; DB 4; Length 271;
 Best Local Similarity 100.0%; Pred. No. 2.7e-116;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCLWEESRLIQTATAAQAQGGQANHPHTAAVVTKEQMLEQHLQDVVRKRVODLEQMKVVE 60
 DB 1 RCLWEESRLIQTATAAQAQGGQANHPHTAAVVTKEQMLEQHLQDVVRKRVODLEQMKVVE 60
 QY 61 NLQDDDFNFKTLKSGQMDLNGNQSQVTRQKMQLEQMLTALDQRRSIVSELAGLLS 120
 DB 61 NLQDDDFNFKTLKSGQMDLNGNQSQVTRQKMQLEQMLTALDQRRSIVSELAGLLS 120
 QY 121 AMEVVOKTLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 180
 DB 121 AMEVVOKTLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 180
 QY 181 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
 DB 181 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
 QY 241 TKVRLVKPELNYQLKIKVICDKSDGVAA 271
 DB 241 TKVRLVKPELNYQLKIKVICDKSDGVAA 271

RESULT 2
 AAR72082
 ID AAR72082 standard; protein; 770 AA.
 XX
 AC AAR72082;
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX
 DE Mouse Stat3 (19sf6).
 XX
 XX Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
 KW receptor recognition factor; transcription factor; cellular debilitation;
 KW derangement; dysfunction; interferon-gamma.
 XX
 OS Mus sp.
 XX
 XX WO9508629-A1.
 PN
 XX
 PD 30-MAR-1995.
 XX
 XX 26-SEP-1994; 94WO-US010849.
 XX
 XX 24-SEP-1993; 93US-00126588.
 PR
 XX 24-SEP-1993; 93US-00126595.
 PR
 XX 11-MAR-1994; 94US-00212184.
 PR
 XX 11-MAR-1994; 94US-00212185.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 PA
 XX Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 PI
 XX WPI; 1995-139598/18.
 DR
 DR N-PSDB; AAQ89340.
 XX
 XX Receptor recognition factor implicated in transcriptional stimulation of
 PT genes - useful in drug screening assays and/or for treating cellular
 PT debilitations, derangements and/or dysfunctions, etc.
 XX

PS Claim 1; Page 107-110; 160pp; English.
 XX
 CC A fragment encoding the human Stat91 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
 CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC -40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed
 CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 770 AA;

Query Match 100.0%; Score 1388; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 1.1e-115;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RCLWEESRLIQTATAAQAQGGQANHPHTAAVVTKEQMLEQHLQDVVRKRVODLEQMKVVE 60
 DB 107 RCLWEESRLIQTATAAQAQGGQANHPHTAAVVTKEQMLEQHLQDVVRKRVODLEQMKVVE 166
 QY 61 NLQDDDFNFKTLKSGQMDLNGNQSQVTRQKMQLEQMLTALDQRRSIVSELAGLLS 120
 DB 167 NLQDDDFNFKTLKSGQMDLNGNQSQVTRQKMQLEQMLTALDQRRSIVSELAGLLS 226
 QY 121 AMEVVOKTLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 180
 DB 227 AMEVVOKTLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESQLOTRQOIKKLEE 286
 QY 181 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 240
 DB 287 LQKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFT 346
 QY 241 TKVRLVKPELNYQLKIKVICDKSDGVAA 271
 DB 347 TKVRLVKPELNYQLKIKVICDKSDGVAA 377

RESULT 3
 AAW03176
 ID AAW03176 standard; protein; 770 AA.
 XX
 AC AAW03176;
 XX
 DT 24-OCT-1996 (first entry)
 DT
 XX
 DE Mouse STAT4.
 XX
 XX STAT; STAT4; signal transducer and activator of transcription;
 KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
 KW autoimmune disease; antagonist; therapy.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH Domain 398..508
 FT /label= DNA binding domain
 FT /note= "Claim 3, page 110"
 XX
 PN WO9620954-A2.
 XX
 XX 11-JUL-1996.
 PD
 XX 28-DEC-1995; 95WO-US017025.
 PF
 XX 06-JAN-1995; 95US-00369796.
 PR
 XX (UYRQ) UNIV ROCKEFELLER.
 PA
 XX Darnell JE, Wen Z, Horvath CM, Zhong Z;
 PI
 XX WPI; 1996-333941/33.
 DR

CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human Stat3
 CC protein
 XX
 SQ Sequence 769 AA;

Query Match 99.2%; Score 1377; DB 5; Length 769;
 Best Local Similarity 99.3%; Pred. No. 1e-114;
 Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQOMLEOHLQDVRKRVQDLQKMKVVE 60
 Db 107 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQOMLEOHLQDVRKRVQDLQKMKVVE 166

Qy 61 NLQDDDFNFKYTKLSQGDMDLNGNOSVTRQKQOQLQMLTALDQWRSTVSELAGLLS 120
 Db 167 NLQDDDFNFKYTKLSQGDMDLNGNOSVTRQKQOQLQMLTALDQWRSTVSELAGLLS 226

Qy 121 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNWNITSLAESQLQTRQIKKLEE 180
 Db 227 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNWNITSLAESQLQTRQIKKLEE 286

Qy 181 LQOKVSYKGDPIVOHRPMLBERIVELFRNLKMSAFVVERQPCMPHDPRLVITGVQFT 240
 Db 287 LQOKVSYKGDPIVOHRPMLBERIVELFRNLKMSAFVVERQPCMPHDPRLVITGVQFT 346

Qy 241 TKVRLLYKFPPELNYQLKIKVICDKSGDVAA 271
 Db 347 TKVRLLYKFPPELNYQLKIKVICDKSGDVAA 377

RESULT 7
 AAEE22056
 ID AAE22056 standard; protein; 769 AA.

XX AAEE22056;
 XX
 XX 25-JUL-2002 (first entry)
 XX Human protein related to angiogenesis regulation.
 DE
 XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.
 XX Homo sapiens.
 OS
 XX WO200220032-A1.
 FN
 XX

PD 14-MAR-2002.
 XX
 XX 10-SEP-2001; 2001WO-US028254.
 XX
 XX 08-SEP-2000; 2000US-0231212P.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 XX Yu H, Pardoll D, Jove R, Dalton W;
 PI WPI; 2002-362218/39.
 DR
 XX Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.
 XX
 XX Disclosure; Page 83-85; 94pp; English.
 XX
 CC The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC protein related to angiogenesis regulation
 XX
 SQ Sequence 769 AA;

Query Match 99.2%; Score 1377; DB 5; Length 769;
 Best Local Similarity 99.3%; Pred. No. 1e-114;
 Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQOMLEOHLQDVRKRVQDLQKMKVVE 60
 Db 107 RCLWEESRLLOTAATAAQGGQANHPPTAAVTEKQOMLEOHLQDVRKRVQDLQKMKVVE 166

Qy 61 NLQDDDFNFKYTKLSQGDMDLNGNOSVTRQKQOQLQMLTALDQWRSTVSELAGLLS 120
 Db 167 NLQDDDFNFKYTKLSQGDMDLNGNOSVTRQKQOQLQMLTALDQWRSTVSELAGLLS 226

Qy 121 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNWNITSLAESQLQTRQIKKLEE 180
 Db 227 AMEVQKTLTDEELADWKRPEIACIGPPNICLDRLNWNITSLAESQLQTRQIKKLEE 286

Qy 181 LQOKVSYKGDPIVOHRPMLBERIVELFRNLKMSAFVVERQPCMPHDPRLVITGVQFT 240
 Db 287 LQOKVSYKGDPIVOHRPMLBERIVELFRNLKMSAFVVERQPCMPHDPRLVITGVQFT 346

Qy 241 TKVRLLYKFPPELNYQLKIKVICDKSGDVAA 271
 Db 347 TKVRLLYKFPPELNYQLKIKVICDKSGDVAA 377

Db	347	TKVLLVFPPELNYQLKIKVCIDKDSGVAA	377
RESULT 8			
AAR82995			
ID	AAR82995	standard; protein; 770 AA.	
XX	AC	AAR82995;	
XX	DT	25-MAR-1996 (first entry)	
XX	DE	Mouse liver acute phase response factor.	
XX	XX	Mouse; acute phase response factor; transcription factor; interleukin-6;	
XX	KW	signal transmission; liver; antibody; antisense; ribozyme;	
XX	KW	antiinflammatory; anticumor; hypotensive; therapy.	
XX	OS	Mus musculus.	
XX	XX	EP676469-A2.	
XX	XX	11-OCT-1995.	
XX	XX	29-MAR-1995; 95EP-00104670.	
XX	XX	04-APR-1994; 94JP-00065825.	
XX	XX	(KISH/) KISHIMOTO T.	
XX	XX	Akira S, Kishimoto T;	
XX	XX	WPI; 1995-346089/45.	
XX	XX	N-PSDB; AAT05619.	
XX	PT	New acute phase response factor - for developing inhibitory agents for	
XX	PT	treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory	
XX	PT	diseases.	
XX	PS	Claim 10; Page 20-22; 31pp; English.	
XX	CC	The sequence represents a mouse acute phase response factor (APRF), a	
XX	CC	transcription factor related to signal transmission of interleukin-6 (IL-	
XX	CC	6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA	
XX	CC	library using a polymerase chain reaction product (amplified using	
XX	CC	primers derived from an IL-6-treated mouse liver peptide) as a probe.	
XX	CC	APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or	
XX	CC	ribozymes, may be used to treat diseases induced by IL-6, e.g.	
XX	CC	inflammatory disease, leukemia, cancer, osteoclasia, pulmonary	
XX	CC	hypertension, etc	
XX	SQ	Sequence 770 AA;	
Qy		Query Match 99.2%; Score 1377; DB 2; Length 770;	
Db		Best Local Similarity 99.3%; Pred. No. 1e-114;	
		Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	RCLWEESRLLOTAATAAQQGGQANHPPTAAVTEKQMLEQHLQDVVRKVQDLEQKMKVVE	60
Db	107	RCLWEESRLLOTAATAAQQGGQANHPPTAAVTEKQMLEQHLQDVVRKVQDLEQKMKVVE	166
Qy	61	NLQDDDFNYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLS	120
Db	167	NLQDDDFNYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLS	226
Qy	121	AMEYVQKTLTDEELADWKRREPEIACIGPPNICLDRLNWNITSLAESQLOTRQIKKLEE	180
Db	227	AMEYVQKTLTDEELADWKRREPEIACIGPPNICLDRLNWNITSLAESQLOTRQIKKLEE	286
Qy	181	LOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT	240
Db	287	LOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT	346
Qy	241	TKVLLVFPPELNYQLKIKVCIDKDSGVAA	271

Db	347	TKVLLVFPPELNYQLKIKVCIDKDSGVAA	377
RESULT 9			
AAY03768			
ID	AAY03768	standard; protein; 770 AA.	
XX	AC	AAY03768;	
XX	DT	11-JUN-1999 (first entry)	
XX	DE	Human STAT3 allelic variant.	
XX	XX	Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;	
XX	KW	intracellular transcription factor; interleukin-6; medicament; variant;	
XX	KW	pharmaceutical; autoimmune disease; inflammatory; human.	
XX	OS	Homo sapiens.	
XX	XX	EP905234-A2.	
XX	XX	31-MAR-1999.	
XX	XX	18-FEB-1998; 98EP-00102774.	
XX	XX	16-SEP-1997; 97EP-00116061.	
XX	XX	(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.	
XX	XX	Serlupi-Crescenzi O, Della Pietra L;	
XX	XX	WPI; 1999-192664/17.	
XX	XX	N-PSDB; AAX29281.	
XX	XX	New human Signal Transducer and Activator of Transcription 3 (STAT3)	
XX	XX	allelic variant useful for treatment of autoimmune and inflammatory	
XX	XX	disease.	
XX	PS	Claim 2; Page 9-13; 32pp; English.	
XX	CC	The present sequence represents a predominant allelic variant of human	
XX	CC	Signal Transducer and Activator of Transcription 3 (STAT3) protein, an	
XX	CC	intracellular transcription factor which mediates IL-6 signals. The	
XX	CC	encoding sequence differs from the original published human STAT3 gene	
XX	CC	sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3	
XX	CC	DNA molecule can be used for the recombinant expression of the variant.	
XX	CC	STAT3 protein is useful as a medicament or pharmaceutical composition for	
XX	CC	treatment of autoimmune or inflammatory diseases	
XX	SQ	Sequence 770 AA;	
Qy		Query Match 99.2%; Score 1377; DB 2; Length 770;	
Db		Best Local Similarity 99.3%; Pred. No. 1e-114;	
		Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	RCLWEESRLLOTAATAAQQGGQANHPPTAAVTEKQMLEQHLQDVVRKVQDLEQKMKVVE	60
Db	107	RCLWEESRLLOTAATAAQQGGQANHPPTAAVTEKQMLEQHLQDVVRKVQDLEQKMKVVE	166
Qy	61	NLQDDDFNYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLS	120
Db	167	NLQDDDFNYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLS	226
Qy	121	AMEYVQKTLTDEELADWKRREPEIACIGPPNICLDRLNWNITSLAESQLOTRQIKKLEE	180
Db	227	AMEYVQKTLTDEELADWKRREPEIACIGPPNICLDRLNWNITSLAESQLOTRQIKKLEE	286
Qy	181	LOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT	240
Db	287	LOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFT	346
Qy	241	TKVLLVFPPELNYQLKIKVCIDKDSGVAA	271

Db 347 TKVRLLVKPELNYQLKIKVCIDKSGDVAA 377

RESULT 10
AAB12377

ID AAB12377 standard; peptide; 770 AA.
XX AAB12377;
XX 08-NOV-2000 (first entry)
DT XX
DE N-terminal domain of murine STAT-3 protein.
XX
KW STAT; signal transducer and activator of transcription; crystal;
drug design; murine.
XX
OS Mus sp.
XX
XX Location/Qualifiers
FH 4..9
Region /label= Alpha helix 1
FT 12..21
Region /label= Alpha helix 2
FT 19..21
Region /label= 3(10) helix of alpha helix 2
FT 28..33
Region /label= Alpha helix 3
FT 35..40
Region /label= Alpha helix 4
FT 43..47
Region /label= Alpha helix 5
FT 50..73
Region /label= Alpha helix 6
FT 77..96
Region /label= Alpha helix 7
FT 99..119
Region /label= Alpha helix 8
XX
XX US6087478-A.
XX
XX 11-JUL-2000.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX
XX WPI; 2000-505108/45.
XX
XX New crystals of an N-terminal fragment of a signal transducer and
activator of transcription that effectively diffracts x-rays, useful for
drug screening and development.
XX
XX Disclosure; Fig 1; 42pp; English.
XX
XX The present invention relates to a crystal of an N-terminal fragment of a
signal transducer and activator of transcription (STAT) protein. The
crystal effectively diffracts x-rays, allowing the determination of the
atomic coordinates of the N-terminal domain to a resolution of greater
than 5.0 Angstroms. The present sequence is the N-terminal domain of the
murine STAT 3 protein. The N-terminal domain enables STAT dimers to
interact and bind DNA cooperatively, a mechanism important for gene
activation. The crystals are useful in drug screening and development by
selecting a potential drug by performing rational drug design with the 3-
dimensional structure determined for the crystal
XX
SQ Sequence 770 AA;
Query Match 99.2%; Score 1377; DB 3; Length 770;

Query Match 99.2%; Score 1377; DB 3; Length 770;

CC the control of a promoter containing at least two adjacent weak binding
 CC sites for STAT protein dimers. The methods are used for identifying new
 CC drugs. An antagonist of STAT N-terminal dimeric interactions that
 CC inhibits the binding of the STAT dimers to adjacent weak binding sites on
 CC a promoter of a gene, could be useful as drugs in the treatment of
 CC diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other
 CC hand, an agonist of N-terminal dimeric interactions between STAT dimers,
 CC can be used as drugs in the treatment of diseases e.g. anaemia,
 CC neutropaenia, thrombocytopaenia, cancer, obesity, viral diseases and
 CC growth retardation. The present sequence is murine STAT3 protein
 XX
 XX Sequence 770 AA;

Query Match 99.2%; Score 1377; DB 5; Length 770;
 Best Local Similarity 99.3%; Pred. No. 1e-114;
 Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQMLEQHLQDVRKRVQDLEQKMKVVE 60
 DB 107 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQMLEQHLQDVRKRVQDLEQKMKVVE 166
 QY 61 NLQDDDFNFYKTLKSGQDMQDLNNGNQSVTRQKMQLEQMLTALDQWRRSIVSELAGLLS 120
 DB 167 NLQDDDFNFYKTLKSGQDMQDLNNGNQSVTRQKMQLEQMLTALDQWRRSIVSELAGLLS 226
 QY 121 AMEYVOKTLTDEELADWKRRPEIACIGGPPNICLDRLNNWITSIAESQLOTRQOIKKLEE 180
 DB 227 AMEYVOKTLTDEELADWKRRPEIACIGGPPNICLDRLNNWITSIAESQLOTRQOIKKLEE 286
 QY 181 LQOKVSKGDPVVOHRPMLERIVELFRNLKMSAFVVERPCMPMPHDPRLVKTGVQFT 240
 DB 287 LQOKVSKGDPVVOHRPMLERIVELFRNLKMSAFVVERPCMPMPHDPRLVKTGVQFT 346
 QY 241 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 271
 DB 347 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 12
 ABG69497
 ID ABG69497 standard; protein; 770 AA.
 XX
 AC ABG69497;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human bait protein STAT3.
 XX
 KW Human; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;
 KW non-insulin diabetes mellitus; obesity; selected interacting domain; SID;
 KW protein-protein interaction map; PIM; anorectic; metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200253726-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 28-DEC-2001; 2001WO-EP015423.
 XX
 PR 02-JAN-2001; 2001US-0259377P.
 XX
 PA (HYBR-) HYBRIGENICS.
 PA (CNRS) CENT NAT RECH SCI.
 XX
 XX Legrain P, Marullo S, Jockers R;
 XX
 XX WPI; 2002-583612/62.
 DR N-PSDB; ABS51033.
 XX
 PT Novel complex of protein-protein interactions in adipocyte cells for
 PT identifying compounds that modulate the protein-protein interactions and
 PT useful for treating obesity and metabolic disorders.

XX
 PS
 XX
 CC Claim 1; Page 54; 125pp; English.
 CC The invention relates to a complex of protein-protein interactions
 CC (forming a protein-protein interaction map, PIM) in adipocyte cells as
 CC defined in the specification, or polynucleotides in adipocytes encoding the
 CC for the polypeptides. Also included are a recombinant cell expressing the
 CC interacting polypeptides and a method of selecting a modulating compound
 CC in adipocyte cells, by cultivating a recombinant host cell on a selective
 CC medium containing a modulating compound and a reporter gene the
 CC expression of which is toxic for the recombinant host cell which is
 CC transformed with two vectors, where the first vector comprises a
 CC polynucleotide encoding a first hybrid polypeptide and DNA binding domain
 CC and the second vector comprising a polynucleotide encoding a second
 CC hybrid polypeptide and an activating domain that activates the toxic
 CC reporter gene, when the first and second hybrid polypeptides interact and
 CC selecting the modulating compound which inhibits the growth of the
 CC recombinant host cell (i.e. using the yeast two-hybrid system). The
 CC complexes are useful for identifying compounds that modulate the protein-
 CC protein interactions and useful for treating obesity and metabolic
 CC disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The
 CC compound isolated by the method is useful for treating and preventing
 CC obesity or metabolic diseases. The interactions between the proteins of
 CC the complex further define a set of selected interacting domains, SID.
 CC The present sequence represents a member of the protein complex of the
 CC invention, used as the bait protein in the yeast two-hybrid assay
 XX
 SQ Sequence 770 AA;

Query Match 99.2%; Score 1377; DB 5; Length 770;
 Best Local Similarity 99.3%; Pred. No. 1e-114;
 Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQMLEQHLQDVRKRVQDLEQKMKVVE 60
 DB 107 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQMLEQHLQDVRKRVQDLEQKMKVVE 166
 QY 61 NLQDDDFNFYKTLKSGQDMQDLNNGNQSVTRQKMQLEQMLTALDQWRRSIVSELAGLLS 120
 DB 167 NLQDDDFNFYKTLKSGQDMQDLNNGNQSVTRQKMQLEQMLTALDQWRRSIVSELAGLLS 226
 QY 121 AMEYVOKTLTDEELADWKRRPEIACIGGPPNICLDRLNNWITSIAESQLOTRQOIKKLEE 180
 DB 227 AMEYVOKTLTDEELADWKRRPEIACIGGPPNICLDRLNNWITSIAESQLOTRQOIKKLEE 286
 QY 181 LQOKVSKGDPVVOHRPMLERIVELFRNLKMSAFVVERPCMPMPHDPRLVKTGVQFT 240
 DB 287 LQOKVSKGDPVVOHRPMLERIVELFRNLKMSAFVVERPCMPMPHDPRLVKTGVQFT 346
 QY 241 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 271
 DB 347 TKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 13
 ABU10476
 ID ABU10476 standard; protein; 770 AA.
 XX
 AC ABU10476;
 XX
 DT 06-AUG-2003 (first entry)
 XX
 DE Mouse STAT3 protein.
 XX
 KW Mouse; signal transducer and activator of transcription; drug design;
 KW drug screening; STAT-STAT dimer interaction; STAT3.
 XX
 OS Mus sp.
 XX
 PH Key
 FT Region 4..9
 FT /label= alpha_helix_1
 FT Region 12..21

```
FT FT /label= alpha_helix_2
FT FT /note= "Residues 19-21 form a 3 helix"
FT FT 28..33
FT FT /label= alpha_helix_3
FT FT 35..40
FT FT /label= alpha_helix_4
FT FT 43..47
FT FT /label= alpha_helix_5
FT FT 50..73
FT FT /label= alpha_helix_6
FT FT /note= "Residues 57, 61, 64, 68 and 71 contribute to
FT FT packing of the coiled-coil"
FT FT 77..96
FT FT /label= alpha_helix_7
FT FT /note= "Residues 79, 83, 86, 90 and 94 contribute to
FT FT packing of the coiled-coil"
FT FT 99..119
FT FT /label= alpha_helix_8
FT FT
XX XX US2003003563-A1.
XX XX
XX XX 02-JAN-2003.
XX XX
XX XX 19-OCT-2001; 2001US-00045792.
XX XX
XX XX 23-JAN-1998; 98US-00012710.
XX XX
XX XX 24-APR-2000; 2000US-00556273.
XX XX
XX XX (VINK/) VINKEMEIER U.
XX XX (MOAR/) MOAREFI I.
XX XX (DARN/) DARNELL J E.
XX XX (KURI/) KURIYAN J.
XX XX
XX XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX XX
XX XX WPI; 2003-447354/42.
XX XX
XX XX New crystal having an N-terminal domain of a STAT protein performing X-
XX XX ray crystallographic studies, useful for screening drugs that enhance or
XX XX inhibit STAT-STAT dimer interactions.
XX XX
XX XX Disclosure; Page 25-26; 46pp; English.
XX XX
XX XX The invention relates to a crystal of an N-terminal domain of signal
XX XX transducer and activator of transcription (STAT) protein, where the
XX XX crystal effectively diffracts X-rays for the determination of the atomic
XX XX coordinates of the N-terminal domain of the STAT protein to a resolution
XX XX of greater than 5.0 Angstrom. The methods and compositions are useful for
XX XX the design and screening of drugs that enhance or inhibit STAT-STAT dimer
XX XX interactions. The present sequence represents the amino acid sequence of
XX XX mouse STAT3 protein
XX XX
XX XX Sequence 770 AA;

Query Match 99.2%; Score 1377; DB 6; Length 770;
Best Local Similarity 99.3%; Pred. No. 1e-114;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RCLWEERLLQTATAAQQGGQANHPHTAAVTEKQMLEQHLQDVRKRVQDLEQKMKVVE 60
Db 107 RCLWEERLLQTATAAQQGGQANHPHTAAVTEKQMLEQHLQDVRKRVQDLEQKMKVVE 166

Qy 61 NLQDDDFNFKYTKLSQGDMDLNGNNSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLS 120
Db 167 NLQDDDFNFKYTKLSQGDMDLNGNNSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLS 226

Qy 121 AMEYVQKTLTDEELADWKRREPEIACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEE 180
Db 167 NLQDDDFNFKYTKLSQGDMDLNGNNSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLS 226

Qy 121 AMEYVQKTLTDEELADWKRREPEIACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEE 180
Db 227 AMEYVQKTLTDEELADWKRREPEIACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEE 286

Qy 181 LQOKSVYKGDPIVOHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVKTGVQFT 240
Db 227 AMEYVQKTLTDEELADWKRREPEIACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLEE 286

Qy 181 LQOKSVYKGDPIVOHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVKTGVQFT 240
Db 287 LQOKSVYKGDPIVOHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVKTGVQFT 346

Qy 241 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 271
Db 347 TKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377
```

RESULT 15
ADP54789
ID ADP54789 standard; protein; 770 AA.
XX
XX AC ADP54789;
XX DT 18-NOV-2004 (first entry)
XX DE Human PRO protein sequence SEQ ID NO:765.
XX KW human; PRO; immune related disease; inflammatory immune response;
KW immune response stimulation; antiallergic; antianaemic; antiarthritic;
KW antiaesthetic; antidiabetic; antiinflammatory; antipsoriatic;
KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW varicide; gene therapy.
XX OS Homo sapiens.
XX DN WO2004039956-A2.
XX PD 13-MAY-2004.
XX PF 28-OCT-2003; 2003WO-US034381.
XX PR 29-OCT-2002; 2002US-0422472P.
XX PA (GETH) GENENTECH INC.
XX PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX WI WI: 2004-376182/35.
DR N-PSDB; ADP54788.
XX New PRO polynucleotides and polypeptides, useful in diagnosing
PT and treating an immune related disease, e.g. systemic lupus
PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
PT stimulating an immune response.
XX
PS Claim 1; SEQ ID NO 765; 3009pp; English.
XX
CC The present invention describes an isolated PRO nucleic acid (1). Also
CC described: (1) a vector comprising (1); (2) a host cell comprising the
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC antibody which specifically binds to a polypeptide of (4); (7) a
CC composition of matter comprising a polypeptide of (4); an agonist or
CC antagonist of the polypeptide or an antibody that binds to the
CC polypeptide in combination with a carrier; (8) an article of manufacture
CC comprising a container, a label on the container and a composition of
CC matter of (7); (9) a method of treating an immune related disease in a
CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC; and (13) a method of stimulating the immune response in a mammal. The
CC PRO sequences have antiallergic, antianaemic, antiarthritic,
CC antiaesthetic, antidiabetic, antiinflammatory, antipsoriatic,
CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC virucide activities, and can be used in gene therapy. The nucleic acid
CC (1) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO protein from the present invention.

SQ Sequence 770 AA;
Query Match 99.2%; Score 1377; DB 8; Length 770;
Best Local Similarity 99.3%; Pred. No. 1e-114;
Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQKQMLEQHLQDVRRKRVODLEQKMKVVE 60
DB 107 RCLWEESRLLOTAATAAQQGGQANHPHTAAVVTKEQKQMLEQHLQDVRRKRVODLEQKMKVVE 166
QY 61 NLODDDFNYKTLKSGODMODLNGNNSQSVTRQKQMLEQMLTALDQWRRSIVSELAGLLS 120
DB 167 NLODDDFNYKTLKSGODMODLNGNNSQSVTRQKQMLEQMLTALDQWRRSIVSELAGLLS 226
QY 121 AMEYVOKTLDDELADWKREPEIACIGGPPNICLDLENWITSIAESQLOTRQOIKKLEE 180
DB 227 AMEYVOKTLDDELADWKRRQOQIACIGGPPNICLDLENWITSIAESQLOTRQOIKKLEE 286
QY 181 LQOKSVYKGDPIVQHRPMLLEERIVELFRNLKMSAFVVERQPCMPMHDPRLVKTGVQFT 240
DB 287 LQOKSVYKGDPIVQHRPMLLEERIVELFRNLKMSAFVVERQPCMPMHDPRLVKTGVQFT 346
QY 241 TKVRLLVKPPPELNYQLKIKVCIDKSGDVAA 271
DB 347 TKVRLLVKPPPELNYQLKIKVCIDKSGDVAA 377

Search completed: May 5, 2005, 15:01:10
Job time : 85.1694 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:14:45 ; Search time 50.566 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-21

Perfect score: 477

Sequence: 1 VQLEQKKVVENLQDDFF.....YVQKLTDELADWKRPEI 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	95	4 AAY72853	Aay72853 Mouse Sta
2	477	100.0	128	4 AAY72852	Aay72852 Mouse Sta
3	477	100.0	143	4 AAY72849	Aay72849 Mouse Sta
4	477	100.0	176	4 AAY72848	Aay72848 Mouse Sta
5	477	100.0	213	4 AAY72851	Aay72851 Mouse Sta
6	477	100.0	223	4 AAY72854	Aay72854 Mouse Sta
7	477	100.0	228	4 AAY72861	Aay72861 Mouse Sta
8	477	100.0	229	4 AAY72860	Aay72860 Mouse Sta
9	477	100.0	229	4 AAY72850	Aay72850 Mouse Sta
10	477	100.0	229	4 AAY72863	Aay72863 Mouse Sta
11	477	100.0	229	4 AAY72862	Aay72862 Mouse Sta
12	477	100.0	236	4 AAY72847	Aay72847 Mouse Sta
13	477	100.0	252	4 AAY72846	Aay72846 Mouse Sta
14	477	100.0	271	4 AAY72841	Aay72841 Mouse Sta
15	477	100.0	770	2 AAY72082	Aay72082 Mouse Sta
16	477	100.0	770	2 AAW03176	Aaw03176 Mouse Sta
17	466	97.7	720	5 AAE22055	Aae22055 Human Sta
18	466	97.7	769	5 ABB57164	Abb57164 Mouse isc
19	466	97.7	769	5 AAE22054	Aae22054 Human Sta
20	466	97.7	769	5 AAE22056	Aae22056 Human pro
21	466	97.7	770	2 AAR82995	Aar82995 Mouse liv
22	466	97.7	770	2 AAR82993	Aar82993 Human pla
23	466	97.7	770	2 AAY03768	Aay03768 Human Sta
24	466	97.7	770	3 AAB12377	Aab12377 N-termina
25	466	97.7	770	4 AAB19964	Aab19964 Human sig

26 466 97.7 770 5 AAE14652 Aae14652 Murine ST
27 466 97.7 770 5 ABG69497 Abg69497 Human bai
28 466 97.7 770 5 AAE15174 Aae15174 Human Sta
29 466 97.7 770 6 ABU10476 Abu10476 Mouse STA
30 466 97.7 770 7 ADD44738 Add44738 Rat Prote
31 466 97.7 770 7 ADD44740 Add44740 Human Pro
32 466 97.7 770 8 ADN04365 Adn04365 Antipsoi
33 466 97.7 770 8 ADP54789 Adp54789 Human PRO
34 466 97.7 793 3 AAB58442 Aab58442 Lung canc
35 278 58.3 185 4 AAY72855 Aay72855 Mouse Sta
36 173 36.3 423 6 ABR47598 Abr47598 Breast ca
37 173 36.3 704 2 AAW01102 Aaw01102 Signal tr
38 173 36.3 748 2 AAW01101 Aaw01101 Signal tr
39 173 36.3 748 4 AAB19965 Aab19965 Human sig
40 173 36.3 748 5 AAE15175 Aae15175 Human Sta
41 173 36.3 748 6 ABR47599 Abr47599 Breast ca
42 173 36.3 748 8 ADL82891 Adl82891 Human PRO
43 173 36.3 748 8 ADP13003 Adp13003 Protein e
44 173 36.3 748 8 ADRI14069 Adri14069 Human NF-
45 173 36.3 748 8 ADRI14361 Adri14361 Human NF-

ALIGNMENTS

RESULT 1

AAY72853

ID AAY72853 standard; protein; 95 AA.

AC AAY72853;

XX 31-MAY-2001 (first entry)

XX Mouse Stat3 protein fragment #11 (155-249 amino acids).

XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dyeproliferative disease; cancer; psoriasis;
KW therapy.

XX Mus musculus.

XX WO200116605-A2.

XX 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US023822.

XX 31-AUG-1999; 99US-00387418.

XX (UYRQ) UNIV ROCKEFELLER.

XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;

XX WPI; 2001-226705/23.

XX Identifying an agent for use in modulating the interaction between
transcription factor c-Jun and a Stat3 protein.

XX Claim 65; Page 78; 86pp; English.

XX The present sequence is mouse Stat3 protein fragment containing 155-249
amino acids of Stat3 protein. The invention relates to methods for
identifying interacting regions of transcription factors and methods for
transformation. These identifying agents are used in the treatment of
CC identifying agents which modulates the interaction between a
transcription factor such as c-Jun and a Stat protein such as Stat-1 and
Stat-3, useful for modulating gene transcription e.g., cellular
transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
binding domain, linker domain, SH2 domain and transactivation domain
XX Sequence 95 AA;

```

Query Match      100.0%; Score 477; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 5.9e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
DB 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60

QY 61 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
DB 61 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95

RESULT 2
AAV72852
ID AAY72852 standard; protein; 128 AA.
XX
AC AAY72852;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #10 (155-282 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
FH Key
FT Region
FT 24..48
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
XX
PN WO200116605-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023822.
XX
PR 31-AUG-1999; 99US-00387418.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
PT Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX
PS Claim 65; Page 78; 86pp; English.
XX
CC The present sequence is mouse Stat3 protein fragment containing 155-282
CC amino acids of Stat3 protein. The invention relates to methods for
CC identifying interacting regions of transcription factors and methods for
CC identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX
SQ Sequence 128 AA;
Query Match      100.0%; Score 477; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 8.3e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
DB 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60

QY 61 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
DB 61 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95

Query Match      100.0%; Score 477; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 9.5e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
DB 49 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 108

QY 61 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
DB 109 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 143

RESULT 4
AAV72848
ID AAY72848 standard; protein; 176 AA.
XX
AC AAY72848;
XX

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```

RESULT 3
AAV72849
ID AAY72849 standard; protein; 143 AA.
XX
AC AAY72849;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #7 (107-249 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
FH Key
FT Region
FT 24..48
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
XX
PN WO200116605-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023822.
XX
PR 31-AUG-1999; 99US-00387418.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
PT Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX
PS Claim 65; Page 75-76; 86pp; English.
XX
CC The present sequence is mouse Stat3 protein fragment containing 107-249
CC amino acids of Stat3 protein. The invention relates to methods for
CC identifying interacting regions of transcription factors and methods for
CC identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX
SQ Sequence 143 AA;
Query Match      100.0%; Score 477; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 9.5e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
DB 49 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 108

QY 61 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
DB 109 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 143

RESULT 4
AAV72848
ID AAY72848 standard; protein; 176 AA.
XX
AC AAY72848;
XX

```


DT 31-MAY-2001 (first entry)
XX Mouse Stat3 protein fragment #6 (107-282 amino acids).
DE
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
XX Mus musculus.
OS
XX
XX
FH Key Location/Qualifiers
FT Region 24..48
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
XX
XX WO200116605-A2.
PN
XX
XX
XX 08-MAR-2001.
PD
XX
XX 30-AUG-2000; 2000WO-US023822.
PF
XX
XX 31-AUG-1999; 99US-00387418.
PR
XX
XX (UYRQ) UNIV ROCKEFELLER.
PA
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
PI WPI; 2001-226705/23.
DR
XX
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
PT
XX
XX Claim 65; Page 74-75; 86pp; English.
PS
XX
XX The present sequence is mouse Stat3 protein fragment containing 107-282
CC amino acids of Stat3 protein. The invention relates to methods for
CC identifying interacting regions of transcription factors and methods for
CC identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX
XX
XX Sequence 176 AA;
Query Match 100.0%; Score 477; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.2e-40;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VODLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
DB 49 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 108
QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
RESULT 5
AAY72851
ID AAY72851 standard; protein; 213 AA.
AC
XX
XX AAY72851;
XX
XX 31-MAY-2001 (first entry)
DT
XX
XX Mouse Stat3 protein fragment #9 (130-342 amino acids).
DE
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.

XX
OS
XX Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT Region 1..25
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
XX
XX WO200116605-A2.
PN
XX
XX
XX 08-MAR-2001.
PD
XX
XX 30-AUG-2000; 2000WO-US023822.
PF
XX
XX 31-AUG-1999; 99US-00387418.
PR
XX
XX (UYRQ) UNIV ROCKEFELLER.
PA
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
PI WPI; 2001-226705/23.
DR
XX
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
PT
XX
XX Claim 65; Page 77; 86pp; English.
PS
XX
XX The present sequence is mouse Stat3 protein fragment containing 130-342
CC amino acids of Stat3 protein. This Stat3 fragment showed very weak
CC binding to c-Jun protein in the cell extract. The invention relates to
CC methods for identifying interacting regions of transcription factors and
CC methods for identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
XX
XX
XX Sequence 213 AA;
Query Match 100.0%; Score 477; DB 4; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-40;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VODLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
DB 26 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLEQMLTALDQMR 85
QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
RESULT 6
AAY72854
ID AAY72854 standard; protein; 223 AA.
AC
XX
XX AAY72854;
XX
XX 31-MAY-2001 (first entry)
DT
XX
XX Mouse Stat3 protein fragment #12 (155-377 amino acids).
DE
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
XX
XX Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT Region 188..204
FT /note= "Stat3-c-Jun interaction region 2; corresponds to

FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 XX
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX
 PS Claim 65; Page 79; 86pp; English.
 XX
 CC The present sequence is mouse Stat3 protein fragment containing 155-377
 CC amino acids of Stat3 protein. The invention relates to methods for
 CC identifying interacting regions of transcription factors and methods for
 CC identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 223 AA;
 Query Match 100.0%; Score 477; DB 4; Length 223;
 Best Local Similarity 100.0%; Pred. No. 1.6e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
 DB 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
 QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
 DB 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
 RESULT 7
 AAY72861
 ID AAY72861 standard; protein; 228 AA.
 XX
 AC AAY72861;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Mouse Stat3 mutant (T346A, K348A, R350A) protein fragment.
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutein.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Region 213..229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 FT Misc-difference 217
 FT /note= "Wild type Thr substituted with Ala; corresponds
 FT to 346 position of Stat-3 protein"

Misc-difference 219
 /note= "Wild type Lys substituted with Ala; corresponds
 to 348 position of Stat-3 protein"
 FT
 FT Misc-difference 221
 /note= "Wild type Arg substituted with Ala; corresponds
 to 350 position of Stat-3 protein"
 FT
 XX WO200116605-A2.
 PN
 XX 08-MAR-2001.
 PD
 XX 30-AUG-2000; 2000WO-US023822.
 XX
 PF 31-AUG-1999; 99US-00387418.
 XX
 PR (UYRQ) UNIV ROCKEFELLER.
 XX
 PA Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 XX
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX
 PS Claim 66; Page 84-85; 86pp; English.
 XX
 CC The present sequence is mouse Stat3 mutant protein fragment containing
 CC 130-358 amino acids of Stat3 protein. This mutant is obtained by
 CC replacing Thr 346 with Ala, Lys 348 with Ala and Arg 350 with Ala in the
 CC Stat3 protein. The invention relates to methods for identifying
 CC interacting regions of transcription factors and methods for identifying
 CC agents which modulates the interaction between a transcription factor
 CC such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for
 CC modulating gene transcription e.g., cellular transformation. These
 CC identifying agents are used in the treatment of dysproliferative diseases
 CC and also for treating cancer and psoriasis. A Stat protein comprises the
 CC N-terminal domain, coiled-coil domain, DNA binding domain, linker domain,
 CC SH2 domain and transactivation domain
 XX
 SQ Sequence 228 AA;
 Query Match 100.0%; Score 477; DB 4; Length 228;
 Best Local Similarity 100.0%; Pred. No. 1.6e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
 DB 25 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 84
 QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
 DB 85 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 119
 RESULT 8
 AAY72860
 ID AAY72860 standard; protein; 229 AA.
 XX
 AC AAY72860;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Mouse Stat3 mutant (L148A, V151A, T346A, K348A, R350A) protein fragment.
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutein.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to

```

FT  Misc-difference 19      130-154 position of Stat3 protein"
FT  /note= "Wild type Leu substituted with Ala; corresponds
FT  to 148 position of Stat-3 protein"
FT  Misc-difference 22
FT  /note= "Wild type Val substituted with Ala corresponds to
FT  151 position of Stat-3 protein"
FT  Region
FT  213..229
FT  /note= "Stat3-c-Jun interaction region 2; corresponds to
FT  342-358 position of Stat3 protein"
FT  Misc-difference 217
FT  /note= "Wild type Thr substituted with Ala corresponds to
FT  346 position of Stat-3 protein"
FT  Misc-difference 219
FT  /note= "Wild type Lys substituted with Ala corresponds to
FT  348 position of Stat-3 protein"
FT  Misc-difference 221
FT  /note= "Wild type Arg substituted with Ala corresponds to
FT  350 position of Stat-3 protein"
XX
PN  WO200116605-A2.
XX
XX  08-MAR-2001.
XX
XX  30-AUG-2000; 2000WO-US023822.
XX
XX  31-AUG-1999; 99US-00387418.
XX  (UYRQ ) UNIV ROCKEFELLER.
XX
XX  Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX  WPI; 2001-226705/23.
XX
XX  Identifying an agent for use in modulating the interaction between
XX  transcription factor c-Jun and a Stat3 protein.
XX
XX  Example 4; Page; 86pp; English.
XX
XX  The present sequence is mouse Stat3 mutant protein fragment containing
XX  130-358 amino acids of Stat3 protein. This mutant is obtained by
XX  replacing Leu 148 with Ala, Val 151 with Ala, Thr 346 with Ala, Lys 348
XX  with Ala and Arg 350 with Ala in the Stat3 protein. The invention relates
XX  to methods for identifying interacting regions of transcription factors
XX  and methods for identifying agents which modulates the interaction
XX  between a transcription factor such as c-Jun and a Stat protein such as
XX  Stat-1 and Stat-3, useful for modulating gene transcription e.g.,
XX  cellular transformation. These identifying agents are used in the
XX  treatment of dysproliferative diseases and also for treating cancer and
XX  psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil
XX  domain, DNA binding domain, linker domain, SH2 domain and transactivation
XX  domain
XX
XX  Sequence 229 AA;
XX
XX  Query Match      100.0%; Score 477; DB 4; Length 229;
XX  Best Local Similarity 100.0%; Pred. No. 1.6e-40;
XX  Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 VQDLEQKMKVVENLQDDFDNFYTKLSQGDMDLNGNNSVTRKMQQLEQMLTALDQMR 60
XX  26 VQDLEQKMKVVENLQDDFDNFYTKLSQGDMDLNGNNSVTRKMQQLEQMLTALDQMR 85
XX
XX  61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
XX  86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
XX
XX  RESULT 9
XX  AAY72850
XX  ID AAY72850 standard; protein; 229 AA.
XX
XX  AAY72850;

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XX  31-MAY-2001 (first entry)
XX
XX  Mouse Stat3 protein fragment #8 (130-358 amino acids).
XX
XX  Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
XX  cellular transformation; dysproliferative disease; cancer; psoriasis;
XX  therapy.
XX
XX  Mus musculus.
XX
XX  Key Location/Qualifiers
XX  Region 1..25
XX  /note= "Stat3-c-Jun interaction region 1; corresponds to
XX  130-154 position of Stat3 protein"
XX  Region 213..229
XX  /note= "Stat3-c-Jun interaction region 2; corresponds to
XX  342-358 position of Stat3 protein"
XX
XX  WO200116605-A2.
XX
XX  08-MAR-2001.
XX
XX  30-AUG-2000; 2000WO-US023822.
XX
XX  31-AUG-1999; 99US-00387418.
XX  (UYRQ ) UNIV ROCKEFELLER.
XX
XX  Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX  WPI; 2001-226705/23.
XX
XX  Identifying an agent for use in modulating the interaction between
XX  transcription factor c-Jun and a Stat3 protein.
XX
XX  Claim 65; Page 76-77; 86pp; English.
XX
XX  The present sequence is mouse Stat3 protein fragment containing 130-358
XX  amino acids of Stat3 protein. This Stat3 fragment showed strong binding
XX  to c-Jun protein in the cell extract. The invention relates to methods
XX  for identifying interacting regions of transcription factors and methods
XX  for identifying agents which modulates the interaction between a
XX  transcription factor such as c-Jun and a Stat protein such as Stat-1 and
XX  Stat-3, useful for modulating gene transcription e.g., cellular
XX  transformation. These identifying agents are used in the treatment of
XX  dysproliferative diseases and also for treating cancer and psoriasis. A
XX  Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
XX  binding domain, linker domain, SH2 domain and transactivation domain
XX
XX  Sequence 229 AA;
XX
XX  Query Match      100.0%; Score 477; DB 4; Length 229;
XX  Best Local Similarity 100.0%; Pred. No. 1.6e-40;
XX  Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 VQDLEQKMKVVENLQDDFDNFYTKLSQGDMDLNGNNSVTRKMQQLEQMLTALDQMR 60
XX  26 VQDLEQKMKVVENLQDDFDNFYTKLSQGDMDLNGNNSVTRKMQQLEQMLTALDQMR 85
XX
XX  61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
XX  86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
XX
XX  RESULT 10
XX  AAY72863
XX  ID AAY72863 standard; protein; 229 AA.
XX
XX  AAY72863;
XX
XX  31-MAY-2001 (first entry)
XX
XX

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DE Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutein.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Misc-difference 22
 FT /note= "Wild type Val substituted with Ala corresponds to
 FT 151 position of Stat-3 protein"
 FT Region 213..229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 PI WPI; 2001-226705/23.
 DR
 XX
 PT Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX
 PS Claim 66; Page 86; 86pp; English.
 XX
 CC The present sequence is mouse Stat3 mutant (V151A) protein fragment
 CC containing 130-358 amino acids of Stat3 protein. This mutant is obtained
 CC by replacing Val 151 with Ala in Stat3 protein. The invention relates to
 CC methods for identifying interacting regions of transcription factors and
 CC methods for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 229 AA;
 Query Match 100.0%; Score 477; DB 4; Length 229;
 Best Local Similarity 100.0%; Pred. No. 1.6e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQDLEQKMKVVENLQDDFDENYKTLKSGQMDLNGNNSQVTRQKMOOLEQMLTALDQMR 60
 DB 26 VQDLEQKMKVVENLQDDFDENYKTLKSGQMDLNGNNSQVTRQKMOOLEQMLTALDQMR 85
 QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
 DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 RESULT 11
 AAY72862
 ID AAY72862 standard; protein; 229 AA.
 XX
 AC AAY72862;
 XX
 DT 31-MAY-2001 (first entry)
 XX

DE Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutein.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Misc-difference 19
 FT /note= "Wild type Leu substituted with Ala; corresponds
 FT to 148 position of Stat-3 protein"
 FT Region 213..229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 PI WPI; 2001-226705/23.
 DR
 XX
 PT Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX
 PS Claim 66; Page 85; 86pp; English.
 XX
 CC The present sequence is mouse Stat3 mutant (L148A) protein fragment
 CC containing 130-358 amino acids of Stat3 protein. This mutant is obtained
 CC by replacing Leu 148 with Ala in Stat3 protein. The invention relates to
 CC methods for identifying interacting regions of transcription factors and
 CC methods for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 229 AA;
 Query Match 100.0%; Score 477; DB 4; Length 229;
 Best Local Similarity 100.0%; Pred. No. 1.6e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQDLEQKMKVVENLQDDFDENYKTLKSGQMDLNGNNSQVTRQKMOOLEQMLTALDQMR 60
 DB 26 VQDLEQKMKVVENLQDDFDENYKTLKSGQMDLNGNNSQVTRQKMOOLEQMLTALDQMR 85
 QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
 DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 RESULT 12
 AAY72847
 ID AAY72847 standard; protein; 236 AA.
 XX
 AC AAY72847;
 XX
 DT 31-MAY-2001 (first entry)
 XX

FT FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT FT 130-154 position of Stat3 protein"
 FT FT 236..252
 FT FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT FT 342-358 position of Stat3 protein"
 PN WO200116605-A2.
 XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 PI WPI; 2001-226705/23.
 DR
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 PT
 XX Claim 65; Page 67-68; 86pp; English.
 XX
 CC The present sequence is mouse Stat3 protein fragment containing 107-377
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 271 AA;
 Query Match 100.0%; Score 477; DB 4; Length 271;
 Best Local Similarity 100.0%; Pred. No. 2e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLTALDQMR 60
 DB 49 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLTALDQMR 108
 QY 61 RSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 95
 DB 109 RSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 143
 RESULT 15
 AAR72082
 ID AAR72082 standard; protein; 770 AA.
 XX
 AC AAR72082;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX
 DE Mouse Stat3 (19sf6).
 XX
 KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
 KW receptor recognition factor; transcription factor; cellular debilitation;
 KW derangement; dysfunction; interferon-gamma.
 XX
 OS Mus sp.
 XX
 PN W09508629-A1.
 XX
 PD 30-MAR-1995.
 XX

PF 26-SEP-1994; 94WO-US010849.
 XX
 PR 24-SEP-1993; 93US-00126588.
 PR 24-SEP-1993; 93US-00126595.
 PR 11-MAR-1994; 94US-00212184.
 PR 11-MAR-1994; 94US-00212185.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 PI WPI; 1995-139598/18.
 DR N-PSDB; AAQ89340.
 XX
 PT Receptor recognition factor implicated in transcriptional stimulation of
 PT genes - useful in drug screening assays and/or for treating cellular
 PT debilitations, derangements and/or dysfunctions, etc.
 XX
 XX Claim 1; Page 107-110; 160pp; English.
 XX
 CC A fragment encoding the human Stat91 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
 CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC -40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed
 CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 770 AA;
 Query Match 100.0%; Score 477; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.8e-40;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLTALDQMR 60
 DB 155 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLTALDQMR 214
 QY 61 RSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 95
 DB 215 RSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 249
 Search completed: May 25, 2005, 17:36:34
 Job time : 58.7327 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 11.8868 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-21
Perfect score: 477
Sequence: 1 VQDLEQMKVVENLQDDDFD.....YVQKLTLDDELADWKRPEI 95

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	95	3	US-09-387-418A-21
2	477	100.0	128	3	US-09-387-418A-20
3	477	100.0	143	3	US-09-387-418A-17
4	477	100.0	176	3	US-09-387-418A-16
5	477	100.0	213	3	US-09-387-418A-19
6	477	100.0	223	3	US-09-387-418A-22
7	477	100.0	229	3	US-09-387-418A-18
8	477	100.0	229	3	US-09-387-418A-28
9	477	100.0	229	3	US-09-387-418A-29
10	477	100.0	229	3	US-09-387-418A-30
11	477	100.0	229	3	US-09-387-418A-31
12	477	100.0	236	3	US-09-387-418A-15
13	477	100.0	252	3	US-09-387-418A-14
14	477	100.0	271	3	US-09-387-418A-9
15	477	100.0	770	1	US-08-369-796-12
16	477	100.0	770	2	US-08-852-091-12
17	477	100.0	770	2	US-08-820-754-12
18	477	100.0	770	3	US-08-956-652-12
19	477	100.0	770	3	US-08-956-869-12
20	477	100.0	770	3	US-08-948-547-12
21	477	100.0	770	3	US-09-364-970-3
22	477	100.0	770	3	US-09-364-970-5
23	477	100.0	770	4	US-08-956-653A-12
24	477	100.0	770	4	US-08-212-185-12
25	477	100.0	770	5	PCT-US95-17025-12
26	466	97.7	770	1	US-08-416-581B-1
27	466	97.7	770	1	US-08-416-581B-5

28	466	97.7	770	1	US-08-416-581B-9	Sequence 9, Appli
29	466	97.7	770	3	US-09-012-710-8	Sequence 8, Appli
30	466	97.7	770	3	US-09-087-465-6	Sequence 6, Appli
31	466	97.7	770	3	US-09-556-273-8	Sequence 8, Appli
32	466	97.7	770	3	US-09-526-542-2	Sequence 2, Appli
33	466	97.7	770	4	US-09-972-800A-6	Sequence 6, Appli
34	466	97.7	770	4	US-10-117-087-2	Sequence 2, Appli
35	466	97.7	771	1	US-08-276-099A-14	Sequence 14, Appl
36	466	97.7	771	1	US-08-781-890-14	Sequence 14, Appl
37	278	58.3	185	3	US-09-387-418A-23	Sequence 23, Appl
38	173	36.3	748	1	US-08-408-318-2	Sequence 2, Appli
39	173	36.3	748	1	US-08-839-164-2	Sequence 2, Appli
40	173	36.3	748	3	US-09-087-465-8	Sequence 8, Appli
41	173	36.3	748	4	US-09-972-800A-8	Sequence 8, Appli
42	170	35.6	749	1	US-08-369-796-8	Sequence 8, Appli
43	170	35.6	749	2	US-08-852-091-8	Sequence 8, Appli
44	170	35.6	749	2	US-08-820-754-8	Sequence 8, Appli
45	170	35.6	749	3	US-08-956-652-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-387-418A-21
; Sequence 21, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-21

Query Match	100.0%	Score	477	DB	3	Length	95
Best Local Similarity	100.0%	Pred. No.	3.8e-45	Mismatches	0	Indels	0
Matches	95	Conservative	0	Indels	0	Gaps	0
QY	1	VQDLEQMKVVENLQDDDFD	FNKTLKSQGDMDLNGNNSVTRQKMQQLTALDQMR	60			
Db	1	VQDLEQMKVVENLQDDDFD	FNKTLKSQGDMDLNGNNSVTRQKMQQLTALDQMR	60			
QY	61	RSIVSELGILLSAMEYVQKLT	DEELADWKRPEI	95			
Db	61	RSIVSELGILLSAMEYVQKLT	DEELADWKRPEI	95			

RESULT 2
US-09-387-418A-20
; Sequence 20, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43

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/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 20
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-387-418A-20

Query Match      100.0%; Score 477; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.5e-45;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
    |||
Db 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
    |||

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
    |||
Db 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
    |||

RESULT 3
US-09-387-418A-17
/ Sequence 17, Application US/09387418A
/ Patent No. 6391572
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Xiaokui
/ APPLICANT: Wrzeszczynska, Melissa H
/ APPLICANT: Horvath, Curt M
/ APPLICANT: Darnell Jr., James E
/ TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
/ TITLE OF INVENTION: INTERACTIONS
/ FILE REFERENCE: 600-1-253
/ CURRENT APPLICATION NUMBER: US/09/387,418A
/ CURRENT FILING DATE: 1999-08-31
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 17
/ LENGTH: 143
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-387-418A-17

Query Match      100.0%; Score 477; DB 3; Length 143;
Best Local Similarity 100.0%; Pred. No. 6.4e-45;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
    |||
Db 49 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 108
    |||

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
    |||
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
    |||

RESULT 4
US-09-387-418A-16
/ Sequence 16, Application US/09387418A
/ Patent No. 6391572
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Xiaokui
/ APPLICANT: Wrzeszczynska, Melissa H
/ APPLICANT: Horvath, Curt M
/ APPLICANT: Darnell Jr., James E
/ TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
/ TITLE OF INVENTION: INTERACTIONS
/ FILE REFERENCE: 600-1-253
/ CURRENT APPLICATION NUMBER: US/09/387,418A
/ CURRENT FILING DATE: 1999-08-31
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 16
/ LENGTH: 176
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/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-387-418A-16

Query Match      100.0%; Score 477; DB 3; Length 176;
Best Local Similarity 100.0%; Pred. No. 8.2e-45;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
    |||
Db 49 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 108
    |||

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
    |||
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
    |||

RESULT 5
US-09-387-418A-19
/ Sequence 19, Application US/09387418A
/ Patent No. 6391572
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Xiaokui
/ APPLICANT: Wrzeszczynska, Melissa H
/ APPLICANT: Horvath, Curt M
/ APPLICANT: Darnell Jr., James E
/ TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
/ TITLE OF INVENTION: INTERACTIONS
/ FILE REFERENCE: 600-1-253
/ CURRENT APPLICATION NUMBER: US/09/387,418A
/ CURRENT FILING DATE: 1999-08-31
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 213
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-387-418A-19

Query Match      100.0%; Score 477; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 60
    |||
Db 26 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQOLEQMLTALDQMR 85
    |||

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
    |||
Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
    |||

RESULT 6
US-09-387-418A-22
/ Sequence 22, Application US/09387418A
/ Patent No. 6391572
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Xiaokui
/ APPLICANT: Wrzeszczynska, Melissa H
/ APPLICANT: Horvath, Curt M
/ APPLICANT: Darnell Jr., James E
/ TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
/ TITLE OF INVENTION: INTERACTIONS
/ FILE REFERENCE: 600-1-253
/ CURRENT APPLICATION NUMBER: US/09/387,418A
/ CURRENT FILING DATE: 1999-08-31
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 22
/ LENGTH: 223
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-387-418A-22
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Query Match      100.0%; Score 477; DB 3; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
Db 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

RESULT 7
US-09-387-418A-18
; Sequence 18, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-18

Query Match      100.0%; Score 477; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
Db 26 VQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLNGNNSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 8
US-09-387-418A-28
; Sequence 28, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-28

Query Match      100.0%; Score 477; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
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Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
Db 26 VQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLNGNNSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 9
US-09-387-418A-29
; Sequence 29, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-29

Query Match      100.0%; Score 477; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
Db 26 VQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLNGNNSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 10
US-09-387-418A-30
; Sequence 30, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-30

Query Match      100.0%; Score 477; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLNGNNSVTRQKMQQLEQMLTALDQMR 60
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Db 26 VQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
|||||
Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

RESULT 11
US-09-387-418A-31
; Sequence 31, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-31

Query Match 100.0%; Score 477; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
Db 26 VQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
|||||
Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

RESULT 12
US-09-387-418A-15
; Sequence 15, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-15

Query Match 100.0%; Score 477; DB 3; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
Db 49 VQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 108
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QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
|||||
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143

RESULT 13
US-09-387-418A-14
; Sequence 14, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-14

Query Match 100.0%; Score 477; DB 3; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
Db 49 VQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 108

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
|||||
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143

RESULT 14
US-09-387-418A-9
; Sequence 9, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-9

Query Match 100.0%; Score 477; DB 3; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.4e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
Db 49 VQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLNGNNSVTRQKMQOLEQMLTALDQMR 108

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
|||||
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143
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RESULT 15
US-08-369-796-12
; Sequence 12, Application US/08369796
; Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-369-796-12

Query Match 100.0%; Score 477; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.1e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 155 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSVTRQKMQQLTALDQMR 214

Qy 61 RSIVSELGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db 215 RSIVSELGLLSAMEYVQKTLTDEELADWKRRPEI 249

Search completed: May 25, 2005, 17:47:37
Job time : 15.8868 secs

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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:36:58 ; Search time 41.6038 Seconds
(without alignments)
763.830 Million cell updates/sec

Title: US-10-090-185-21
Perfect score: 477
Sequence: 1 VQDLEQKMKVVENLQDDFDF.....YVQKTLTDEELADWKRRPEI 95

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	477	100.0	95	US-10-090-185-21	Sequence 21, Appl
2	477	100.0	128	US-10-090-185-20	Sequence 20, Appl
3	477	100.0	143	US-10-090-185-17	Sequence 17, Appl
4	477	100.0	176	US-10-090-185-16	Sequence 16, Appl
5	477	100.0	213	US-10-090-185-19	Sequence 19, Appl
6	477	100.0	223	US-10-090-185-22	Sequence 22, Appl
7	477	100.0	229	US-10-090-185-18	Sequence 18, Appl
8	477	100.0	229	US-10-090-185-28	Sequence 28, Appl
9	477	100.0	229	US-10-090-185-29	Sequence 29, Appl
10	477	100.0	229	US-10-090-185-30	Sequence 30, Appl
11	477	100.0	229	US-10-090-185-31	Sequence 31, Appl
12	477	100.0	236	US-10-090-185-15	Sequence 15, Appl
13	477	100.0	252	US-10-090-185-14	Sequence 14, Appl

14	477	100.0	271	13	US-10-090-185-9	Sequence 9, Appl
15	477	100.0	770	11	US-09-876-773-12	Sequence 12, Appl
16	477	100.0	770	17	US-10-639-617-12	Sequence 12, Appl
17	466	97.7	720	15	US-10-380-020-4	Sequence 4, Appl
18	466	97.7	769	15	US-10-380-020-2	Sequence 2, Appl
19	466	97.7	769	15	US-10-380-020-5	Sequence 5, Appl
20	466	97.7	770	14	US-10-045-792-8	Sequence 8, Appl
21	466	97.7	770	14	US-10-038-010-56	Sequence 56, Appl
22	466	97.7	770	14	US-10-117-087-2	Sequence 2, Appl
23	466	97.7	770	15	US-10-116-275-329	Sequence 329, App
24	466	97.7	770	15	US-10-116-275-349	Sequence 349, App
25	466	97.7	793	9	US-09-925-302-780	Sequence 780, App
26	466	97.7	793	10	US-09-925-302-780	Sequence 23, Appl
27	278	58.3	185	13	US-10-090-185-23	Sequence 437, App
28	173	36.3	423	14	US-10-177-293-437	Sequence 439, App
29	173	36.3	748	14	US-10-177-293-439	Sequence 70, Appl
30	173	36.3	748	16	US-10-755-889-70	Sequence 362, App
31	173	36.3	748	16	US-10-755-889-362	Sequence 6, Appl
32	170	35.6	749	9	US-09-833-205-6	Sequence 8, Appl
33	170	35.6	749	11	US-09-876-773-8	Sequence 8, Appl
34	170	35.6	749	14	US-10-045-792-7	Sequence 7, Appl
35	170	35.6	749	14	US-10-205-194-39	Sequence 39, Appl
36	170	35.6	749	17	US-10-639-617-8	Sequence 8, Appl
37	168	35.2	749	9	US-09-833-205-4	Sequence 4, Appl
38	160.5	33.6	749	14	US-10-045-792-9	Sequence 9, Appl
39	158	33.1	268	13	US-10-090-185-12	Sequence 12, Appl
40	158	33.1	582	14	US-10-245-120-3	Sequence 3, Appl
41	158	33.1	712	11	US-09-876-773-6	Sequence 6, Appl
42	158	33.1	712	14	US-10-245-120-2	Sequence 2, Appl
43	158	33.1	712	17	US-10-639-617-6	Sequence 6, Appl
44	158	33.1	712	17	US-10-639-617-6	Sequence 5, Appl
45	158	33.1	750	9	US-09-833-205-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-090-185-21
; Sequence 21, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 21
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-21

Query Match 100.0%; Score 477; DB 13; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.8e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VQDLEQKMKVVENLQDDFDFNYKTLKSGQMDQNLGNQSVTRQKMQOLEMLTALDQMR 60
DB 1 VQDLEQKMKVVENLQDDFDFNYKTLKSGQMDQNLGNQSVTRQKMQOLEMLTALDQMR 60
QY 61 RSTVSLAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 61 RSTVSLAGLLSAMEYVQKTLTDEELADWKRRPEI 95

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RESULT 2
US-10-090-185-20
; Sequence 20, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-20

Query Match      100.0%; Score 477; DB 13; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.6e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VQLEQKMKVVENLQDDDFENYKTLKSGQMDLNGNNSQSVTRKMQQLEQMLTALDQMR 60

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

RESULT 3
US-10-090-185-17
; Sequence 17, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-17

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Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 49 VQLEQKMKVVENLQDDDFENYKTLKSGQMDLNGNNSQSVTRKMQQLEQMLTALDQMR 108

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
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RESULT 4
US-10-090-185-16
; Sequence 16, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-16

Query Match      100.0%; Score 477; DB 13; Length 176;
Best Local Similarity 100.0%; Pred. No. 3.8e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 49 VQLEQKMKVVENLQDDDFENYKTLKSGQMDLNGNNSQSVTRKMQQLEQMLTALDQMR 108

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143

RESULT 5
US-10-090-185-19
; Sequence 19, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-19

Query Match      100.0%; Score 477; DB 13; Length 213;
Best Local Similarity 100.0%; Pred. No. 4.8e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 26 VQLEQKMKVVENLQDDDFENYKTLKSGQMDLNGNNSQSVTRKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
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Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 6

US-10-090-185-22

; Sequence 22, Application US/10090185

; Publication No. US20020197647A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzrzeszczynska, Melissa H

; APPLICANT: Horvath, Curt M

; APPLICANT: Darnell Jr., James E

; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

; FILE REFERENCE: 600-1-253

; CURRENT APPLICATION NUMBER: US/10/090,185

; CURRENT FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: 09/387,418

; PRIOR FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 22

; LENGTH: 223

; TYPE: PRT

; ORGANISM: Mus musculus

; US-10-090-185-22

Query Match 100.0%; Score 477; DB 13; Length 223;

Best Local Similarity 100.0%; Pred. No. 5.1e-42;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSQSVTRQKMQQLEQMLTALDQMR 60

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

Db 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

RESULT 7

US-10-090-185-18

; Sequence 18, Application US/10090185

; Publication No. US20020197647A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzrzeszczynska, Melissa H

; APPLICANT: Horvath, Curt M

; APPLICANT: Darnell Jr., James E

; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

; FILE REFERENCE: 600-1-253

; CURRENT APPLICATION NUMBER: US/10/090,185

; CURRENT FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: 09/387,418

; PRIOR FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Mus musculus

; US-10-090-185-18

Query Match 100.0%; Score 477; DB 13; Length 229;

Best Local Similarity 100.0%; Pred. No. 5.3e-42;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 26 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSQSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 8

US-10-090-185-28

; Sequence 28, Application US/10090185

; Publication No. US20020197647A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzrzeszczynska, Melissa H

; APPLICANT: Horvath, Curt M

; APPLICANT: Darnell Jr., James E

; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

; FILE REFERENCE: 600-1-253

; CURRENT APPLICATION NUMBER: US/10/090,185

; CURRENT FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: 09/387,418

; PRIOR FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 28

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Mus musculus

; US-10-090-185-28

Query Match 100.0%; Score 477; DB 13; Length 229;

Best Local Similarity 100.0%; Pred. No. 5.3e-42;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSQSVTRQKMQQLEQMLTALDQMR 60

Db 26 VQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNNSQSVTRQKMQQLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95

Db 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

RESULT 9

US-10-090-185-29

; Sequence 29, Application US/10090185

; Publication No. US20020197647A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzrzeszczynska, Melissa H

; APPLICANT: Horvath, Curt M

; APPLICANT: Darnell Jr., James E

; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

; FILE REFERENCE: 600-1-253

; CURRENT APPLICATION NUMBER: US/10/090,185

; CURRENT FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: 09/387,418

; PRIOR FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 29

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Mus musculus

; US-10-090-185-29

Query Match 100.0%; Score 477; DB 13; Length 229;

Best Local Similarity 100.0%; Pred. No. 5.3e-42;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

RESULT 10

US-10-090-185-30
; Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-30

Query Match 100.0%; Score 477; DB 13; Length 229;
Best Local Similarity 100.0%; Pred. No. 5.3e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQMKVVENLQDDFDNFYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
DB 26 VQDLEQMKVVENLQDDFDNFYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

RESULT 11

US-10-090-185-31
; Sequence 31, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-31

Query Match 100.0%; Score 477; DB 13; Length 229;
Best Local Similarity 100.0%; Pred. No. 5.3e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQMKVVENLQDDFDNFYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
DB 26 VQDLEQMKVVENLQDDFDNFYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 85

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
DB 86 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

RESULT 12

US-10-090-185-15
; Sequence 15, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-15

Query Match 100.0%; Score 477; DB 13; Length 236;
Best Local Similarity 100.0%; Pred. No. 5.5e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQMKVVENLQDDFDNFYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
DB 49 VQDLEQMKVVENLQDDFDNFYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 108

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95
DB 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143

RESULT 13

US-10-090-185-14
; Sequence 14, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14

Query Match 100.0%; Score 477; DB 13; Length 252;
Best Local Similarity 100.0%; Pred. No. 5.9e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQMKVVENLQDDFDNFYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
DB 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143

Db 49 VQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 108

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
|||||
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143

RESULT 14

US-10-090-185-9
; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR P
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-9

Query Match 100.0%; Score 477; DB 13; Length 271;
Best Local Similarity 100.0%; Pred. No. 6.5e-42;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
|||||
Db 49 VQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 108

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
|||||
Db 109 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143

RESULT 15

US-09-876-773-12
; Sequence 12, Application US/09876773
; Publication No. US20040058318A1
; GENERAL INFORMATION:

APPLICANT: Darnell Jr., James E.
Fu, Xian-Yuan
Wen, Zilong
Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match 100.0%; Score 477; DB 11; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.4e-41;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 60
|||||
Db 155 VQDLEQKMKVVENLQDDFDFNYKTLKSQGMQDLNGNNSVTRQKMQOLEQMLTALDQMR 214
QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
|||||
Db 215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249

Search completed: May 25, 2005, 18:21:48
Job time : 53.9371 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:24:07 ; Search time 8.96226 Seconds
(without alignments)
1019.898 Million cell updates/sec

Title: US-10-090-185-21
Perfect score: 477
Sequence: 1 VQDLQKMKVVENLQDDDFD.....YVQKTLTDELDADWKRPEI 95

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	97.7	770	2 A54444	DNA-binding protei
2	466	97.7	770	2 I49508	ISGF3 p91-related
3	164	34.4	748	2 A56047	gamma-interferon a
4	158	33.1	739	2 A46159	interferon-depende
5	93	19.5	786	2 I49274	mammary gland fact
6	93	19.5	793	2 S54772	mammary gland fact
7	89	18.7	794	2 G02317	transcription acti
8	88	18.4	794	2 S55527	mammary gland fact
9	86	18.0	533	2 G72593	hypothetical prote
10	85.5	17.9	2094	2 S33124	tpr protein - huma
11	84.5	17.7	217	2 G75219	hypothetical prote
12	84.5	17.7	821	2 T24728	hypothetical prote
13	83.5	17.5	3187	2 JCS5837	364K Golgi complex
14	82	17.2	1818	1 S73852	hypothetical prote
15	81.5	17.1	217	2 B71203	hypothetical prote
16	79.5	16.7	278	2 AC3354	hypothetical prote
17	79	16.6	638	2 S67605	hypothetical prote
18	78	16.4	1968	1 S05697	myosin heavy chain
19	77.5	16.2	1160	2 I40589	paraspinal crystal
20	77	16.1	304	2 AD1029	probable membrane
21	77	16.1	569	2 B71902	hypothetical prote
22	76.5	16.0	441	2 T01613	hypothetical prote
23	76	15.9	821	2 S67087	hypothetical prote
24	75.5	15.8	734	2 T27055	hypothetical prote
25	75.5	15.8	1085	2 F96712	hypothetical prote
26	75	15.7	742	1 S86591	kinesin-related pr
27	75	15.7	750	2 T38435	coiled coil protei
28	75	15.7	896	2 S43074	epidermal growth f
29	75	15.7	1171	2 T45706	chromosome-associa

30 74.5 15.6 1979 1 S03166 myosin heavy chain
31 74 15.5 412 2 S07537 myosin heavy chain
32 74 15.5 621 2 S10450 myosin heavy chain
33 73.5 15.4 398 2 AC1763 peptidoglycan lyti
34 73.5 15.4 927 2 AG1739 transmembrane prot
35 73.5 15.4 980 2 E71606 hypothetical prote
36 73 15.3 764 2 I51302 myosin heavy chain
37 73 15.3 1526 2 T41522 myosin ii - fisio
38 73 15.3 1738 2 T14867 interaptin - slime
39 72.5 15.2 986 2 T10754 cis-Golgi matrix p
40 72.5 15.2 1046 2 T42734 cytoplasmic linker
41 72.5 15.2 1133 2 T22976 hypothetical prote
42 72.5 15.2 2024 2 A54103 centrosome autoant
43 72 15.1 173 2 JCS610 tropinin I - sea s
44 72 15.1 262 2 JC1237 apolipoprotein A-I
45 72 15.1 264 2 S22420 apolipoprotein A-I

ALIGNMENTS

RESULT 1
A54444
DNA-binding protein APRP - human
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: A54444
R:Akita, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994
A:Title: Molecular cloning of APRP, a novel IFN-stimulated gene factor 3 p91-related tr
A:Reference number: A54444; MUID:94208062; PMID:7512451
A:Accession: A54444
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-770 <RES>
A:Cross-references: UNIPROT:P40763; GB:L29277; NID:G475788; PID:G475789
C:Genetics:
A:Gene: GDB:STAT3; APRF
A:Cross-references: GDB:358950
A:Map position: 17q21-17q21
A:Superfamily: human signal transducer and transcription activator STAT5A
C:Keywords: DNA binding; transcription factor

Query Match 97.7%; Score 466; DB 2; Length 770;
Best Local Similarity 97.9%; Pred. NO. 1.3e-31;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 VQDLQKMKVVENLQDDDFDFFNYKTLKSGQMDLNGNQSVTQKMQOLEQMLTALDOMR 60
Db 155 VQDLQKMKVVENLQDDDFDFFNYKTLKSGQMDLNGNQSVTQKMQOLEQMLTALDOMR 214
Qy 61 RSTVSELGALLSAMEYVQKTLTDELDADWKRPEI 95
Db 215 RSTVSELGALLSAMEYVQKTLTDELDADWKRPEI 249

RESULT 2
I49508
ISGF3 p91-related transcription factor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49508; I49009
R:Akita, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994
A:Title: Molecular cloning of APRP, a novel IFN-stimulated gene factor 3 p91-related tr
A:Reference number: A54444; MUID:94208062; PMID:7512451
A:Accession: I49508
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-770 <RES>
A:Cross-references: UNIPROT:P42227; GB:L29278; NID:G476715; PID:AAA37254.1; PID:G47671
R:Raz, R.; Durbin, J.E.; Levy, D.E.
J. Biol. Chem. 269, 24391-24395, 1994

A>Title: Acute phase response factor and additional members of the interferon-stimulated
A/Reference number: I49009; MUID:95014185; PMID:7523373
A/Accession: I49009
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-393, 'M', 395-700, 702-770 <RE2>
A/Cross-references: EMBL:U08378; NID:9473889; PIDN:AAA5668.1; PID:9473890
C/Genetics:
C/Superfamily: human signal transducer and transcription activator STAT5A

Query Match 97.7%; Score 466; DB 2; Length 770;
Best Local Similarity 97.9%; Pred. No. 1.3e-31;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLNGNNSQVTRQKMQQLEQMLTALDQMR 60
DB 155 VQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLNGNNSQVTRQKMQQLEQMLTALDQMR 214

QY 61 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
DB 215 RSIVSELAGLLSMEYVQKTLTDEELADWKRRQOI 249

RESULT 3
A56047
gamma-interferon activation site-binding protein Stat4 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C/Accession: A56047
R/Famamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, M.; Cell. Biol. 14, 4342-4349, 1994
A/Title: Stat4, a novel gamma interferon activation site-binding protein expressed in ea
A/Reference number: A56047; MUID:94277038; PMID:8007943
A/Accession: A56047
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-748 <YAM>
A/Cross-references: UNIPROT:P42228; GB:U09351; NID:G509502; PIDN:AAA19692.1; PID:G509503
C/Superfamily: human signal transducer and transcription activator STAT5A
C/Keywords: DNA binding; phosphoprotein

Query Match 34.4%; Score 164; DB 2; Length 748;
Best Local Similarity 35.1%; Pred. No. 2.8e-06;
Matches 34; Conservative 26; Mismatches 29; Indels 8; Gaps 2;

QY 1 VQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLNGNNSQVTRQKMQQLEQMLTALDQ 58
DB 154 VQTEQDTKYLEDLQDEFYRYKTIQTMQDQ-----KNSILVQEVLTQLQEMLSLDF 207

QY 59 MRSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
DB 208 KRKEALSKMTQIVNETDLLNMSLLEELQDWKRRQOI 244

RESULT 4
A46159
interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
C/Species: Homo sapiens (man)
C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A46159
R/Schindler, C.; Fu, X.Y.; Imbrota, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 90, 7836-7839, 1992
A/Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG
A/Reference number: A46159; MUID:92366557; PMID:1502203
A/Accession: A46159
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid; protein
A/Residues: 1-739 <SCH>
A/Cross-references: UNIPROT:P42224
A/Experimental source: HeLa cells
A/Note: sequence extracted from NCBI backbone (NCBIP:110818)
C/Superfamily: human signal transducer and transcription activator STAT5A

Query Match 33.1%; Score 158; DB 2; Length 739;
Best Local Similarity 36.2%; Pred. No. 8.9e-06;
Matches 34; Conservative 22; Mismatches 36; Indels 2; Gaps 1;

QY 1 VQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLNGNNSQVTRQKMQQLEQMLTALDQMR 60
DB 153 VMCIEHETKSLELDQDEYDFKCKTL--QNVREHETNGVAKSDQKQBQLLLKKMYLLMDNKR 210

QY 61 RSIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 94
DB 211 KEVHKITIELNVLTETQNALINDELVEWKRQOQ 244

RESULT 5
I49274
mammary gland factor - mouse
N/Alternate names: STAT5 protein homolog p80
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I49274; S54773; S54727
R/Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A/Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved
A/Reference number: I49273; MUID:96004632; PMID:7568026
A/Accession: I49274
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-786 <RNU>
A/Cross-references: UNIPROT:P42232; UNIPROT:Q9JYK1; EMBL:U21110; NID:9747973; PIDN:AACS
R/Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995
A/Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A/Reference number: S54772; MUID:95237158; PMID:7720707
A/Accession: S54773
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-432, 'E', 434-786 <MUI>
A/Cross-references: EMBL:248539; NID:G758635; PIDN:CAA88420.1; PID:G758636
R/Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,
EMBO J. 14, 1402-1411, 1995
A/Title: Interleukin-3 signals through multiple isoforms of Stat5.
A/Reference number: S54725; MUID:95246733; PMID:7537213
A/Accession: S54727
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-432, 'E', 434-786 <AZA>
C/Genetics:
A/Gene: Stat5b
C/Superfamily: human signal transducer and transcription activator STAT5A

Query Match 19.5%; Score 93; DB 2; Length 786;
Best Local Similarity 26.4%; Pred. No. 2.7;
Matches 28; Conservative 18; Mismatches 48; Indels 12; Gaps 3;

QY 2 QDLEQKMKVVENLQDDDFNY-KTLKSGQDMQDLNGNN-----QSVTRQKMQQLEQML 53
DB 156 QDTENELKKLQQTQYFIQYQESLRIOAQFALGQLNPQBRMSRETAQQKQVSLTTL 215

QY 54 -----TALDQMRSRIVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
DB 216 QREAQTLQYRVLAERKHQTLQLLRKQQTIIILDELIQWKRQOL 261

RESULT 6
S54772
mammary gland factor - mouse
N/Alternate names: stat5 protein
C/Species: Mus musculus (house mouse)
C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C/Accession: S54772; I49273
R/Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.
EMBO J. 14, 1166-1175, 1995

A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin
A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Accession: S54772
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-793 <MUI>
A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIA0; EMBL:Z48538; NID:g758633; PIDN:CAA88
R;Lin, X.; Robinson, G.W.; Guilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A;Title: Cloning and expression of Stats and an additional homologue (Stat5b) involved in
A;Reference number: I49273; MUID:96004632; PMID:7568026
A;Accession: I49273
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-793 <RES>
A;Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972
C;Genetics:
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 19.5%; Score 93; DB 2; Length 793;
Best Local Similarity 26.4%; Pred. No. 2.7;
Matches 28; Conservative 18; Mismatches 48; Indels 12; Gaps 3;

QY 2 QDLEQKMKVVENLQDDFDNY-KTLKSGQDMQDLNGNN-----OSVTRKMQQLEQML 53
DB 156 QDTNELKKLQQTQYFIITQYQESLRQAQFAQLAQLNQPQERLSRETALQQKQVSLAWL 215

QY 54 ----TALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 216 QREAQTLQYRVLEAEKHQKTLQLLRKQQTIIILDDDELQWRRQQL 261

RESULT 7
G02317
transcription activator stat5A - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02317
R;Lin, J.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:gl151169; PIDN:AA806589.1; PID:gl15
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 18.7%; Score 89; DB 2; Length 794;
Best Local Similarity 25.5%; Pred. No. 6;
Matches 27; Conservative 19; Mismatches 48; Indels 12; Gaps 3;

QY 2 QDLEQKMKVVENLQDDFDNY-KTLKSGQDMQDL-----NGNOSVTRKMQQLEQML 53
DB 156 QDTNELKKLQQTQYFIITQYQESLRQAQFAQLAQLNQPQERLSRETALQQKQVSLAWL 215

QY 54 ----TALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 216 QREAQTLQYRVLEAEKHQKTLQLLRKQQTIIILDDDELQWRRQQL 261

RESULT 8
S5527
mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S5527; S44353
R;Wakao, H.; Guilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regula
A;Reference number: S55527; MUID:95188889; PMID:7882987
A;Accession: S55527

A;Molecule type: mRNA
A;Residues: 1-794 <WAK>
A;Cross-references: UNIPROT:P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g602
A;Note: this is a revision to the sequence from reference S44353
R;Wakao, H.; Guilleux, F.; Groner, B.
EMBO J. 13, 2182-2191, 1994
A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcr
A;Reference number: S44353; MUID:94244619; PMID:7514531
A;Accession: S44353
A;Molecule type: mRNA
A;Residues: 1-716, 'RHLGPGSLPSR', 729, 'P', 731, 'ASL', <WAW>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 18.4%; Score 88; DB 2; Length 794;
Best Local Similarity 27.2%; Pred. No. 7.2;
Matches 28; Conservative 16; Mismatches 47; Indels 12; Gaps 3;

QY 2 QDLEQKMKVVENLQDDFDNY-KTLKSGQDMQDLNGNN-----OSVTRKMQQLEQML 53
DB 157 QDTNELKKLQQTQYFIITQYQESLRQAQFAQLAQLNQPQERLSRETALQQKQVSLAWL 216

QY 54 ----TALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 92
DB 217 QREAQTLQYRVLEAEKHQKTLQLLRKQQTIIILDDDELQWRR 259

RESULT 9
G72593
hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72593
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72593
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-533 <KAW>
A;Cross-references: UNIPROT:Q9YCP2; DBJ:AP000061; NID:g5104821; PIDN:BAAB0205.1; PID:d
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1216

Query Match 18.0%; Score 86; DB 2; Length 533;
Best Local Similarity 22.5%; Pred. No. 6.9;
Matches 23; Conservative 27; Mismatches 32; Indels 20; Gaps 3;

QY 1 VODLEQKMKVVEN---LQDDF-----DFNYKTLKSGQDMQDLNGNQSV 41
DB 337 VEDLEARVGSVBRLSQAEEIDSLTSLDSLTLELELSTRLAQAQSLIEDLNLRLDQV 396

QY 42 TRQKMQQLEQMLTALDQWRRSIVSELAGLLSAMEYVQKTLTD 83
DB 397 A-STLQQLQORLATAEESLQALTDLASLQAEVETLQQSIVE 437

RESULT 10
S33124
tpr protein - human
N;Alternate names: kinase-related transforming protein (tpr-met); protein with promoter
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S33124; S23740; S00928; G01185
R;Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 2329-2333, 1992
A;Title: The human tpr gene encodes a protein of 2094 amino acids that has extensive co
A;Reference number: S33124; MUID:93064711; PMID:1437155
A;Accession: S33124

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-2094 <MIT>
A;Cross-references: UNIPROT:Q15624; UNIPROT:Q9UE33; EMBL:X66397; NID:g633225
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
R;Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 383-388, 1992
A;Title: Nucleotide sequence analysis of human tpr cDNA clones.
A;Reference number: S23740; MUID:92195670; PMID:1549355
A;Accession: S23740
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-725, 'L' <MI2>
A;Cross-references: EMBL:X63105; NID:g37257; PIDN:CAA44819.1; PID:g37258
R;King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.
Oncogene 2, 617-619, 1988
A;Title: Tpr homologues activate met and raf.
A;Reference number: S00928; MUID:88262257; PMID:3387099
A;Accession: S00928
A;Molecule type: mRNA
A;Residues: 1-31, 'R', 33-142 <KIN>
A;Cross-references: EMBL:Y00672; NID:g37255; PIDN:CAA68681.1; PID:g37256
R;Greco, A.
submitted to the EMBL Data Library, December 1995
A;Reference number: H00592
A;Accession: G01185
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 144-228 <GRE>
A;Cross-references: EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; PID:g1296798
C;Genetics:
A;Gene: GDB:TPR
A;Cross-references: GDB:128821; OMIM:189940
A;Map position: 1q25-1q25
A;Introns: 177/3

Query Match 17.9%; Score 85.5; DB 2; Length 2094;
Best Local Similarity 26.5%; Pred. No. 33;
Matches 26; Conservative 24; Mismatches 21; Indels 27; Gaps 4;

QY 3 DLEQKMKV---VENLQDDFDNFYKTLKSK-----GDMQDLNGNNSVTRQKMQ 47
DB 1423 DIQEKVKTITQVKIGRRYQTVQELKAQDKVMTSAQSSGDHQE-----QHVSVQEMQ 1477

QY 48 QLEQMLTALDQMRSSIVSELAGLLSAMEYVQKLTDEE 85
DB 1478 ELKETLNQAEATKSKLSQ-----VENLQKTLSEKE 1508

RESULT 11

G75219
hypothetical protein PAB2166 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G75219
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A;Reference number: A75001
A;Accession: G75219
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <KAW>
A;Cross-references: UNIPROT:Q9V122; GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CA84920
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB2166

Query Match 17.7%; Score 84.5; DB 2; Length 217;
Best Local Similarity 24.0%; Pred. No. 3.6;
Matches 23; Conservative 31; Mismatches 31; Indels 11; Gaps 3;

QY 1 VQDLEQKMKVVENLQDDFD--FNYKTLKSGDMQDLNGNNSVTRQKMQLEMLTALDQM 59

DB 132 LLELKRKVRLEVDLDFHLKXQLIKQEGOLE-----MAREYIKLLEGVRHIDNI 183
QY 60 RRSIVSELAGLLSAMEYVQKLTDEELADWKERPEI 95
DB 184 KANVETLLSGYLE--DVIRKIVNDELNARGLKRTPI 217

RESULT 12

T24728
hypothetical protein T09A5.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24728
R;Lightning, J.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19928
A;Accession: T24728
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-821 <WIL>
A;Cross-references: UNIPROT:P45970; EMBL:Z36753; PIDN:CAA85342.1; GSPDB:GNO0020; CESP:T
A;Experimental source: clone T09A5
C;Genetics:
A;Gene: CESP:T09A5.10
A;Map position: 2
A;Introns: 47/2; 253/2; 604/3; 643/1; 712/3

Query Match 17.7%; Score 84.5; DB 2; Length 821;
Best Local Similarity 23.9%; Pred. No. 15;
Matches 27; Conservative 22; Mismatches 31; Indels 33; Gaps 3;

QY 2 QDLEQKMKVVENLQDDFDNFYKTLKSGDMQDLNG-----NNQSVTRQKMQ 47
DB 318 ENLTAKLKTVT-----EDNGKMKQARELDNDYEFARFROEQELTTLRATQDMA 371

QY 48 QLEQMLTALDQMRSSIVSELAGLLSAMEYV-----QKLTDEELA 87
DB 372 DLQELTGVKEIRASLKSENEISASVEELSVASLRNKQADNSKTMLSELA 424

RESULT 13

JC5837
364K Golgi complex-associated protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: JC5837
R;Toki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Y.; Ikehara, Y.
Cell Struct. Funct. 22, 565-577, 1997
A;Title: Identification and characterization of rat 364-kDa Golgi-associated protein re
A;Reference number: JC5837; MUID:98093490; PMID:9431462
A;Accession: JC5837
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-3187 <ROK>
A;Cross-references: UNIPROT:Q63714; DBJ:D25543; NID:9516825; PIDN:BAA05026.1; PID:g516
C;Comment: This protein plays a role in the formation and maintenance of the characteri
C;Superfamily: Gintin
F;49-549,624-1176,1238-1707,1763-3114/Domain: coiled-coil leucine zipper #status predic
F;3165-3187/Domain: membrane anchor #status predicted <MAD>

Query Match 17.5%; Score 83.5; DB 2; Length 3187;
Best Local Similarity 25.5%; Pred. No. 76;
Matches 26; Conservative 17; Mismatches 40; Indels 19; Gaps 2;

QY 3 DLEQKMKVVENLQDDFDNFYKTLKSGDMQDLNGNNSVTRQKMQLEMLTALDQ----- 58
DB 150 ELQKEKLIISNLOAQDLQAOSEQASOLDKSAEMEDFILMRQKLOEKKEELIGALQOTLSQ 209

QY 59 -----MERSIVSE---LAGLLSAMEYVQKLTDEE 85
DB 210 TQAEQAAQKURVMQKLEEHHEALLGRAQVVDLLQKELTSAE 251

Search completed: May 25, 2005, 17:45:23
Job time : 12.9623 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:15:30 ; Search time 39.5283 Seconds
(without alignments)
1230.701 Million cell updates/sec

Title: US-10-090-185-21

Perfect score: 477

Sequence: 1 VQDLQKMKVENVLQDDDF.....YVQKTLTDELADWKRPEI 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	466	97.7	770	1	STA3_HUMAN	P40763 homo sapien
2	466	97.7	770	1	STA3_MOUSE	P42227 mus musculus
3	466	97.7	770	1	STA3_RAT	P52631 rattus norv
4	459	96.2	770	1	STA3_BOVIN	P61635 bos taurus
5	451	94.5	771	2	Q6DV79	Q6dv79 gallus gall
6	440.5	92.3	108	2	Q704W6	Q704w6 bos taurus
7	432	90.6	769	2	Q9PVX8	Q9pvx8 xenopus lae
8	427	89.5	766	2	Q7ZXK3	Q7zxk3 oryzias lat
9	381	79.9	765	2	Q6DVF3	Q6dgv3 oryzias lat
10	379	79.5	785	2	Q6GUE7	Q6gue7 oryzias lat
11	379	79.5	414	2	Q7ZTS5	Q7zts5 brachydanio
12	379	79.5	786	2	Q6NV46	Q6nv46 brachydanio
13	379	79.5	806	2	Q93599	Q93599 brachydanio
14	375	78.6	767	2	O13133	O13133 oncorhynch
15	374	78.4	764	2	Q90Y16	Q90y16 tetraodon f
16	173	36.3	748	1	STA4_HUMAN	Q14765 homo sapien
17	170	35.6	712	2	Q99K94	Q99k94 mus musculus
18	170	35.6	749	1	STA1_MOUSE	P42225 mus musculus
19	170	35.6	749	2	Q8C3V4	Q8c3v4 mus musculus
20	170	35.6	749	2	Q8C497	Q8c497 mus musculus
21	170	35.6	749	2	Q9D323	Q9d323 mus musculus
22	170	35.6	755	2	Q8C8M3	Q8c8m3 mus musculus
23	169	35.4	757	2	Q764M5	Q764m5 mus scrofa
24	168	35.2	712	2	Q6P6Q7	Q6p6q7 rattus norv
25	168	35.2	737	2	Q90Y15	Q90y15 tetraodon f
26	168	35.2	749	2	Q9QXK0	Q9qxk0 rattus norv
27	168	35.2	1165	2	Q7TP57	Q7tp57 rattus norv
28	163	34.2	657	2	Q8AW24	Q8aw24 brachydanio
29	162.5	34.1	718	2	Q801Y2	Q801y2 carassius a
30	161	33.8	748	2	Q66HB2	Q66hb2 rattus norv
31	160.5	33.6	749	1	STA4_MOUSE	P42228 mus musculus

32	158	33.1	750	1	STA1_HUMAN	P42224 homo sapien
33	158	33.1	750	2	Q68D00	Q68d00 homo sapien
34	156	32.7	752	2	Q8JF08	Q8jff8 brachydanio
35	155	32.5	751	2	Q8JGNO	Q8jgn0 xenopus lae
36	154	32.3	651	2	Q7Z253	Q7z253 brachydanio
37	154	32.3	667	2	Q8AW20	Q8aw20 brachydanio
38	153.5	32.2	652	2	Q7Z277	Q7z277 brachydanio
39	153	32.1	553	2	Q8JF07	Q8jff7 brachydanio
40	147	30.8	754	2	O13131	O13131 oncorhynch
41	146	30.6	749	2	O93598	O93598 brachydanio
42	146	30.6	749	2	Q6P943	Q6p943 brachydanio
43	134	28.1	754	2	O13132	O13132 oncorhynch
44	123	25.8	758	2	Q90Y17	Q90y17 tetraodon f
45	121	25.4	1153	2	Q8JF55	Q8jff5 brachydanio

ALIGNMENTS

RESULT 1	STA3_HUMAN	STANDARD;	PRT;	770 AA.
ID	STA3_HUMAN	STANDARD;	PRT;	770 AA.
AC	P40763; O14916; Q9BW54;			
DT	01-EEB-1995 (Rel. 31, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Signal transducer and activator of transcription 3 (Acute-phase response factor).			
DE	Name=STAT3; Synonyms=APRF;			
OS	Homo sapiens (Human)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Placenta;			
RX	MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;			
RA	Yoshida K., Sudo Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,			
RT	"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling pathway.";			
RT	Cell 77:63-71(1994).			
RN	[2]			
RN	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;			
RA	Della Pietra L., Bresan A., Pezzotti A., Serlupi-Crescenzi O.;			
RT	"Highly conserved amino-acid sequence between murine STAT3 and a revised human STAT3 sequence.";			
RL	Gene 213:119-124(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.			
RA	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,			
RA	Rajkumar N., Yi Q., Nickerson D.A.;			
RT	"SeattlesNfcs. NHLBI HL66862 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).			
RC	TISSUE=Kidney, and Pancreas;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M.J., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN SEQUENCE OF 564-704 FROM N.A.
RN RP
RN TSUVE=Liver;
RN RC
RN Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;
RN Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RN PHOSPHORYLATION ON SERINE.
RN RX MEDLINE=95215843; PubMed=7701321;
RN RA Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
RN "Requirement of serine phosphorylation for formation of STAT-promoter
RN complexes";
RN Science 267:1990-1994(1995).
RN [7]
RN INTERACTION WITH NCOAL.
RN RP PubMed=11773079; DOI=10.1074/jbc.M111486200;
RN RA Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
RN "Functional interaction of STAT3 transcription factor with the
RN coactivator NcoA/SRC1a";
RN J. Biol. Chem. 277:8004-8011(2002).
RN CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
RN (IL-6)-responsive elements identified in the promoters of various
RN acute-phase protein genes.
RN CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
RN CC -1- SUBUNIT: Forms a homodimer or a heterodimer with NCOAL.
RN CC member (at least STAT1). Interacts with NCOAL.
RN CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
RN in response to phosphorylation.
RN CC -1- ALTERNATIVE PRODUCTS:
RN CC Event-Alternative splicing; Named isoforms=2;
RN CC Name=1;
RN CC IsoId=P40763-1; Sequence=Displayed;
RN CC Name=Del-701;
RN CC IsoId=P40763-2; Sequence=VSP_010474;
RN CC -1- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
RN muscle, kidney and pancreas.
RN CC -1- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
RN LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
RN is important for the formation of stable DNA-binding STAT3
RN homodimers and maximal transcriptional activity.
RN CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
RN CC -1- SIMILARITY: Contains 1 SH2 domain.
RN -----
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RN -----
RN EMBL; L29277; AAA58374.1; -;
RN EMBL; AJ012463; CAA10032.1; -;
RN EMBL; AY572796; AAS66986.1; -;
RN EMBL; BC000627; AAH00627.1; -;
RN EMBL; BC014482; AAH14482.1; -;
RN EMBL; AF029311; AAB84254.1; -;
RN FIR; A54444; A54444.
RN HSSP; P42227; 1BG1.
RN TRANSFAC; T01493; -;
RN Genew; HGNC:11364; STAT3.
RN H-InvDB; HIX0013840; -;
RN MIM; 102582; -;
RN GO; GO:0005737; Cytoplasm; TAS.
RN GO; GO:0005634; C:nucleus; TAS.
RN GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. . .); TAS.

DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
DR GO; GO:0000122; P:negative regulation of transcription from P. . .; TAS.
DR GO; GO:0000739; P:neurogenesis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008967; P53 like DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
KW Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
FT DOMAIN 580 670
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (by similarity).
FT VARSPLIC 701 701 Missing (in isoform Del-701).
FT FTID=VSP_010474.
FT VARIANT 32 32 O -> K (in dbSNP:1803125).
FT FTID=VAR_018683.
FT VARIANT 143 143 M -> I.
FT CONFLICT 288 288 /FTID=VAR_018679.
FT CONFLICT 460 460 Q -> H (in Ref. 1).
FT CONFLICT 548 548 P -> S (in Ref. 1).
FT CONFLICT 561 561 K -> N (in Ref. 1).
FT CONFLICT 667 667 F -> Y (in Ref. 1).
FT CONFLICT 730 730 V -> L (in Ref. 1).
FT CONFLICT 730 730 T -> A (in Ref. 1).
SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
Query Match 97.7%; Score 466; DB 1; Length 770;
Best Local Similarity 97.9%; Pred. No. 2.4e-31;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNQSVTQKMQQLTALDQMR 60
DB 155 VQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNQSVTQKMQQLTALDQMR 214
QY 61 RSTVSELAGLLSAMEYVQKTLTDEELADWKKRPEI 95
DB 215 RSTVSELAGLLSAMEYVQKTLTDEELADWKKRQOI 249
RESULT 2
STAJ_MOUSE STANDARD; PRT; 770 AA.
ID STAJ_MOUSE AC P42227;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
DE response factor).
GN Name=Stat3; Synonyms=Aprf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
RN RP AND 632-640.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
RT "Molecular cloning of APRE, a novel IFN-stimulated gene factor 3 p91-
RT related transcription factor involved in the gp130-mediated signaling
RT pathway";
RL Cell 77:63-71(1994).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM STAT3A).


```

FT VARSPLIC 716 770 TTCSNTIDLPMSPTLDSLMQFGNGEGARPSAGGQFESLT
FT FMDLITSECATSPM -> FIDAVWK (in isoform
FT Stat3B).
FT /Ftid=VSP_006287.
FT Missing (in isoform Del-701).
FT /Ftid=VSP_010475.
FT S->A: Decreased transcriptional
FT activation.
FT CONFLICT 16 16 E->K (in Ref. 2).
FT CONFLICT 25 25 M -> T (in Ref. 2 and 4).
FT CONFLICT 394 394 M -> I (in Ref. 1).
FT HELIX 139 180
FT TURN 181 182
FT TURN 197 198
FT HELIX 199 237
FT TURN 238 238
FT HELIX 239 251
FT TURN 252 253
FT HELIX 261 290
FT TURN 294 295
FT TURN 297 301
FT HELIX 302 320
FT STRAND 321 328
FT TURN 330 331
FT TURN 333 334
FT TURN 336 337
FT TURN 338 340
FT STRAND 341 342
FT STRAND 343 351

Query Match 97.7%; Score 466; DB 1; Length 770;
Best Local Similarity 97.9%; Pred. No. 2.4e-31;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLFQMLTALDQMR 60
DB 155 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLFQMLTALDQMR 214

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRQOI 249

RESULT 3
STA3 RAT STANDARD; PRT; 770 AA.
AC P52631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name=Stat3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSU=Liver;
RX MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998;
RA Ripberger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,
RA Fey G.H.;
RT "Transcription factors Stat3 and Stat5b are present in rat liver
RT nuclei late in an acute phase response and bind interleukin-6 response
RT elements."
RL J. Biol. Chem. 270:29998-30006(1995).
CC -1- FUNCTION: Transcription factor that binds to the promoters of various
CC (TL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes.
CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus

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CC in response to phosphorylation (By similarity).
CC -1- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSP-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity (By similarity).
CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X91810; CAA62920.1; -.
CC DR HSSP; P42227; 1BG1.
CC DR RGD; 3772; Stat3.
CC DR InterPro; IPR008967; P53_like_DNA_bnd.
CC DR InterPro; IPR000980; SH2_
CC DR InterPro; IPR001217; STAT.
CC DR Pfam; PF00017; SH2; 1.
CC DR Pfam; PF01017; STAT_alpha; 1.
CC DR Pfam; PF02864; STAT_bind; 1.
CC DR Pfam; PF02865; STAT_int; 1.
CC DR SMART; SM00252; SH2; 1.
CC DR PROSITE; PS50001; SH2; 1.
CC KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
CC Transcription regulation.
CC FT DOMAIN 580 670 SH2.
CC FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
CC FT MOD_RES 727 727 Phosphoserine (By similarity).
CC SQ SEQUENCE 770 AA; 88039 MW; D74A0C76954754ED CRC64;

Query Match 97.7%; Score 466; DB 1; Length 770;
Best Local Similarity 97.9%; Pred. No. 2.4e-31;
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLFQMLTALDQMR 60
DB 155 VQLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNNSVTRQKMQQLFQMLTALDQMR 214

QY 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 95
DB 215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRRQOI 249

RESULT 4
STA3 BOVIN STANDARD; PRT; 770 AA.
AC P61635;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name=Stat3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSU=Mammary gland;
RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
RT "The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus
RT during ruminant evolution."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transcription factor that binds to the promoters of various
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes (By similarity).
CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.

```

CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least START1). Interacts with NCOAL (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation (By similarity).
 CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; AJ620655; CAP06182.1; -
 DR PROSITE; PS50001; SH2; 1.
 KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
 KW Transcription regulation.
 FT DOMAIN 580 670 SH2.
 FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 FT MOD_RES 727 727 Phosphoserine (By similarity).
 SQ SEQUENCE 770 AA; 87974 MW; 9CEB147C73B83274 CRC64;

Query Match 96.2%; Score 459; DB 1; Length 770;
 Best Local Similarity 96.8%; Pred. No. 9.4e-31;
 Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKQMLEQMLTALDQMR 60
 DB 155 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKQMLEQMLTALDQMR 214

QY 61 RSTVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
 DB 215 RSTVSELAGLLSMEYVQKTLTDEELADWKRRQOI 249

RESULT 5
 Q6DV79 ID Q6DV79 PRELIMINARY; PRT; 771 AA.
 AC Q6DV79;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Signal transducer and activator of transcription 3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou G.Y., Leung F.C.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY641397; AAT64887.1; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR00980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR PROSITE; PS50001; SH2; 1.
 SQ SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;

Query Match 94.5%; Score 451; DB 2; Length 771;
 Best Local Similarity 94.7%; Pred. No. 4.5e-30;
 Matches 90; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKQMLEQMLTALDQMR 60
 DB 155 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKQMLEQMLTALDQMR 214
 QY 61 RSTVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
 DB 215 RSTVSELAGLLSMEYVQKTLTDEELADWKRRQOI 249

RESULT 6

Q704W6 ID Q704W6 PRELIMINARY; PRT; 108 AA.
 AC Q704W6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Signal transducer and activator of transcription 3 (Fragment).
 GN Names=stat3;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RI TISSUE=Mammary gland;
 RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ620660; CAP06187.1; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF01017; STAT_alpha; 1.
 DR NON_TER 1
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 12552 MW; 9961C28E59085803 CRC64;

Query Match 92.3%; Score 440.5; DB 2; Length 108;
 Best Local Similarity 96.8%; Pred. No. 4.1e-30;
 Matches 90; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 3 DLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKQMLEQMLTALDQMR 62
 DB 1 DLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKQMLEQMLTALDQMR 59

QY 63 IVSELAGLLSMEYVQKTLTDEELADWKRRPEI 95
 DB 60 IVSELAGLLSMEYVQKTLTDEELADWKRRQOI 92

RESULT 7

Q9PVX8 ID Q9PVX8 PRELIMINARY; PRT; 769 AA.
 AC Q9PVX8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Stat 3.
 GN Name=stat 3;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
 RA Nishinakamura R., Matsumoto Y., Matsuda T., Arizumi T., Heike T.,
 RA Asashima M., Yokota T.;

RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
 embryos independent of BMP-4."
 RL Dev. Biol. 216:481-490(1999).
 DR EMBL; AB017701; BAA86061.1; -.
 DR HSSP; P42227; IBG1.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS00001; SH2; 1.
 SQ SEQUENCE 769 AA; 87974 MW; 0905C03263303069 CRC64;
 Query Match 90.6%; Score 432; DB 2; Length 769;
 Best Local Similarity 88.4%; Pred. No. 1.9e-28;
 Matches 84; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKMQQLTALDQMR 60
 Db |||||
 155 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKMQQLTALDQMR 214
 QY 61 RSIVSELAGLSAMEYVQKLTDEELADWKRPEI 95
 Db |||||
 215 RTIISDLASLLSAMEYVQKLTDEELADWKRQOI 249
 RESULT 8
 Q7ZXK3 PRELIMINARY; PRT; 766 AA.
 ID Q7ZXK3
 AC Q7ZXK3
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Stat3-A protein.
 GN Name=stat3-A;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 CX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richardson S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC044717; AAH44717.1; -.
 DR HSSP; P42227; IBG1.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS00001; SH2; 1.
 SQ SEQUENCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;
 Query Match 89.5%; Score 427; DB 2; Length 766;
 Best Local Similarity 87.4%; Pred. No. 5e-28;
 Matches 83; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKMQQLTALDQMR 60
 Db |||||
 155 VQLEQKMKVVENLQDDFDNFYKTLKSGQMDLNGNNSVTRQKMQQLTALDQMR 214
 QY 61 RSIVSELAGLSAMEYVQKLTDEELADWKRPEI 95
 Db |||||
 215 RTIISDLASLLSAMEYVQKLTDEELADWKRQOI 249
 RESULT 9
 Q6DVF3 PRELIMINARY; PRT; 765 AA.
 ID Q6DVF3
 AC Q6DVF3
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Signal transducer and activation of transcription factor 3.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 CX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu R., Hong Y.;
 RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY639947; AAT64912.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT_alpha; 1.

Thu May 26 10:41:27 2005

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smillus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RA EMBL; BC068320; AAH68320.1; -.
RA ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00001; SH2; 1.
SQ SEQUENCE 786 AA; 90039 MW; FC7371D0B0E5447E CRC64;

Query Match 79.5%; Score 379; DB 2; Length 786;
Best Local Similarity 77.3%; Pred. No. 6.2e-24;
Matches 75; Conservative 14; Mismatches 6; Indels 2; Gaps 2;

QY 1 VODLEQKVKVENLODDFDNFYKTLKSGQDM-QDLNGNQ-SVTQRKMQOLEMLTALDQ 58
DB 154 VQDMEQKMKLENLQDDFDNFYKTLKSGAGLSQDLNGNSQAAATRKMSQLEQMLSDQ 213
QY 59 MRRSIVSELAGLSAMEYVQKTLTDEELADWKRPEI 95
DB 214 LRRQIVTEMAGLSAMDFVQKNLTDEELADWKRQOI 250

RESULT 14
O13133 PRELIMINARY; PRT; 767 AA.
ID O13133
AC O13133;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat3.
GN Name=rbtStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RA EMBL; U60333; AAB60926.1; -.
RX HSP; P42227; IEG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smillus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RA EMBL; BC068320; AAH68320.1; -.
RA ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00001; SH2; 1.
SQ SEQUENCE 786 AA; 90039 MW; FC7371D0B0E5447E CRC64;

Query Match 79.5%; Score 379; DB 2; Length 786;
Best Local Similarity 77.3%; Pred. No. 6.2e-24;
Matches 75; Conservative 14; Mismatches 6; Indels 2; Gaps 2;

QY 1 VODLEQKVKVENLODDFDNFYKTLKSGQDM-QDLNGNQ-SVTQRKMQOLEMLTALDQ 58
DB 154 VQDMEQKMKLENLQDDFDNFYKTLKSGAGLSQDLNGNSQAAATRKMSQLEQMLSDQ 213
QY 59 MRRSIVSELAGLSAMEYVQKTLTDEELADWKRPEI 95
DB 214 LRRQIVTEMAGLSAMDFVQKNLTDEELADWKRQOI 250

RESULT 13
O93599 PRELIMINARY; PRT; 806 AA.
ID O93599
AC O93599;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smillus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RA EMBL; BC068320; AAH68320.1; -.
RA ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00001; SH2; 1.
SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;

Query Match 79.5%; Score 379; DB 2; Length 806;
Best Local Similarity 77.3%; Pred. No. 6.4e-24;
Matches 75; Conservative 14; Mismatches 6; Indels 2; Gaps 2;

QY 1 VODLEQKVKVENLODDFDNFYKTLKSGQDM-QDLNGNQ-SVTQRKMQOLEMLTALDQ 58
DB 154 VQDMEQKMKLENLQDDFDNFYKTLKSGAGLSQDLNGNSQAAATRKMSQLEQMLSDQ 213
QY 59 MRRSIVSELAGLSAMEYVQKTLTDEELADWKRPEI 95
DB 214 LRRQIVTEMAGLSAMDFVQKNLTDEELADWKRQOI 250

RESULT 14
O13133 PRELIMINARY; PRT; 767 AA.
ID O13133
AC O13133;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat3.
GN Name=rbtStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RA EMBL; U60333; AAB60926.1; -.
RX HSP; P42227; IEG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;
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Query Match 78.6%; Score 375; DB 2; Length 767;
Best Local Similarity 75.3%; Pred. No. 1.3e-23;
Matches 73; Conservative 17; Mismatches 5; Indels 2; Gaps 2;

QY 1 VQDLEQKMKVENLQDDDFNYKTLKSQGDQDMLNGNNO-SVTROKMQOQLTALDQ 58
Db 154 VQDMEQKMKWLENLQDDDFNYKTLKSQGLSODMNGNSQAARQKMSQLEQLSALDQ 213

QY 59 MRRSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 95
Db 214 LRRQIVTEMAGLLSAMDVFQKNTLDDDELADWKRRQOI 250

RESULT 15

Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -;
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FFE18BEFD8BE CRC64;

Query Match 78.4%; Score 374; DB 2; Length 764;
Best Local Similarity 76.3%; Pred. No. 1.6e-23;
Matches 74; Conservative 14; Mismatches 7; Indels 2; Gaps 2;

QY 1 VQDLEQKMKVENLQDDDFNYKTLKSQGDQDMLNGNNO-SVTROKMQOQLTALDQ 58
Db 154 VQDMEQKMKWLENLQDDDFNYKTLKSQGLSODMNGNSQAARQKMSQLEQLSALDQ 213

QY 59 MRRSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 95
Db 214 LRRQIVTEMAGLLTAMDYVQKNTLNEELADWKRRQOI 250

Search completed: May 25, 2005, 17:43:41
Job time : 44.5283 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:14:45 ; Search time 68.6634 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-24

Perfect score: 669
Sequence: 1 IACIGPPNICLDRLNWLIT.....LNYQLKIKVICDKSDGVAA 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	669	100.0	129	4 AAY72856	Aay72856 Mouse Sta
2	669	100.0	185	4 AAY72855	Aay72855 Mouse Sta
3	669	100.0	223	4 AAY72854	Aay72854 Mouse Sta
4	669	100.0	271	4 AAY72841	Aay72841 Mouse Sta
5	669	100.0	720	5 AAE22055	Aae22055 Human Sta
6	669	100.0	769	5 ABB57164	Abb57164 Mouse isc
7	669	100.0	769	5 AAE22054	Aae22054 Human Sta
8	669	100.0	769	5 AAE22056	Aae22056 Human pro
9	669	100.0	770	2 AAR72082	Aar72082 Mouse liv
10	669	100.0	770	2 AAR82995	Aar82995 Mouse liv
11	669	100.0	770	2 AAW03176	Aaw03176 Mouse STA
12	669	100.0	770	2 AAY03768	Aay03768 Human STA
13	669	100.0	770	3 AAB12377	Aab12377 N-termina
14	669	100.0	770	5 AAE14652	Aae14652 Murine ST
15	669	100.0	770	5 ABG69497	Abg69497 Human bai
16	669	100.0	770	6 ABU10476	Abu10476 Mouse STA
17	669	100.0	770	8 ADN04365	Adn04365 Antipeori
18	669	100.0	770	8 ADP54789	Adp54789 Human PRO
19	669	100.0	793	3 AAB58442	Aab58442 Lung canc
20	666	99.6	770	7 ADD44738	Add44738 Rat Prote
21	664	99.3	770	2 AAR82993	Aar82993 Human pla
22	664	99.3	770	4 AAB19964	Aab19964 Human sig
23	664	99.3	770	5 AAE15174	Aae15174 Human Sta
24	664	99.3	770	7 ADD44740	Add44740 Human Pro
25	571	85.4	228	4 AAY72861	Aay72861 Mouse Sta

26	571	85.4	229	4 AAY72850	Aay72850 Mouse Sta
27	571	85.4	229	4 AAY72863	Aay72863 Mouse Sta
28	571	85.4	229	4 AAY72862	Aay72862 Mouse Sta
29	571	85.4	252	4 AAY72846	Aay72846 Mouse Sta
30	554	82.8	229	4 AAY72860	Aay72860 Mouse Sta
31	494	73.8	96	4 AAY72857	Aay72857 Mouse Sta
32	493	73.7	213	4 AAY72851	Aay72851 Mouse Sta
33	493	73.7	236	4 AAY72847	Aay72847 Mouse Sta
34	436	65.2	268	4 AAY72844	Aay72844 Mouse Sta
35	436	65.2	582	2 AAW62996	Aaw62996 Human tru
36	436	65.2	582	6 ABU04748	Abu04748 Human exp
37	436	65.2	582	8 ADH57036	Adh57036 Truncated
38	436	65.2	680	6 ABR59713	AbR59713 Human sig
39	436	65.2	712	2 AAR72079	Aar72079 Human STA
40	436	65.2	712	2 AAW03170	Aaw03170 Human STA
41	436	65.2	712	2 AAW62995	Aaw62995 Human STA
42	436	65.2	712	6 ABU04747	Abu04747 Human exp
43	436	65.2	712	6 ABU04735	Abu04735 Human exp
44	436	65.2	712	6 ABU04745	Abu04745 Human exp
45	436	65.2	712	6 ABU04743	Abu04743 Human exp

ALIGNMENTS

RESULT 1
AAY72856
ID AAY72856 standard; protein; 129 AA.
XX
AC AAY72856;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #14 (249-377 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
PH Key
FT Region
FT 94...110
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX
PN WQ200116605-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023822.
XX
PR 31-AUG-1999; 99US-00387418.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
PT Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX
PS Claim 65; Page 80-81; 86pp; English.
XX
CC The present sequence is mouse Stat3 protein fragment containing 249-377
CC amino acids of Stat3 protein. The invention relates to methods for
CC identifying interacting regions of transcription factors and methods for
CC identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A

CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 129 AA;

Query Match 100.0%; Score 669; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 4.2e-69;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQOKVSYKGDPIVQHRPMLER 60
 DB 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQOKVSYKGDPIVQHRPMLER 60
 QY 61 IVELFNLKMSAFVVERQPCMPHDPRLVIKTVGQFTTKVRLLVKFPPELNYOLKIKVCI 120
 DB 61 IVELFNLKMSAFVVERQPCMPHDPRLVIKTVGQFTTKVRLLVKFPPELNYOLKIKVCI 120
 QY 121 DKDSGDVAA 129
 DB 121 DKDSGDVAA 129

RESULT 2
 AAY72855
 ID AAY72855 standard; protein; 185 AA.
 AC AAY72855;
 XX 31-MAY-2001 (first entry)
 DT Mouse Stat3 protein fragment #13 (193-377 amino acids).
 DE
 XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 OS Mus musculus.
 XX
 XX
 PH Key Location/Qualifiers
 FT Region 150..166
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 XX WO200116605-A2.
 PN 08-MAR-2001.
 PD 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 PI WPI; 2001-226705/23.
 DR Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX Claim 65; Page 80; 86pp; English.
 XX The present sequence is mouse Stat3 protein fragment containing 193-377
 CC amino acids of Stat3 protein. The invention relates to methods for
 CC identifying interacting regions of transcription factors and methods for
 CC identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX

SQ Sequence 185 AA;
 Query Match 100.0%; Score 669; DB 4; Length 185;
 Best Local Similarity 100.0%; Pred. No. 6.8e-69;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQOKVSYKGDPIVQHRPMLER 60
 DB 57 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQOKVSYKGDPIVQHRPMLER 116
 QY 61 IVELFNLKMSAFVVERQPCMPHDPRLVIKTVGQFTTKVRLLVKFPPELNYOLKIKVCI 120
 DB 117 IVELFNLKMSAFVVERQPCMPHDPRLVIKTVGQFTTKVRLLVKFPPELNYOLKIKVCI 176
 QY 121 DKDSGDVAA 129
 DB 177 DKDSGDVAA 185

RESULT 3
 AAY72854
 ID AAY72854 standard; protein; 223 AA.
 AC AAY72854;
 XX 31-MAY-2001 (first entry)
 DT Mouse Stat3 protein fragment #12 (155-377 amino acids).
 DE
 XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 OS Mus musculus.
 XX
 XX
 PH Key Location/Qualifiers
 FT Region 188..204
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 XX WO200116605-A2.
 PN 08-MAR-2001.
 PD 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 PI WPI; 2001-226705/23.
 DR Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX Claim 65; Page 79; 86pp; English.
 XX The present sequence is mouse Stat3 protein fragment containing 155-377
 CC amino acids of Stat3 protein. The invention relates to methods for
 CC identifying interacting regions of transcription factors and methods for
 CC identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 223 AA;
 Query Match 100.0%; Score 669; DB 4; Length 223;

Best Local Similarity 100.0%; Pred. No. 8.7e-69; Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVSYGKDPVQHRPMLER 60
 DB 95 IACIGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVSYGKDPVQHRPMLER 154

QY 61 IVELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
 DB 155 IVELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 214

QY 121 DKDSGDVAA 129
 DB 215 DKDSGDVAA 223

RESULT 4
 AAY72841
 ID AAY72841 standard; protein; 271 AA.
 XX AAY72841;
 XX 31-MAY-2001 (first entry)
 XX Mouse Stat3 protein fragment #2 (107-377 amino acids).
 XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX Mus musculus.
 XX Key Location/Qualifiers
 FT Region 24..48
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Region 236..252
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX WO200116605-A2.
 XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX Claim 65; Page 67-68; 86pp; English.
 XX The present sequence is mouse Stat3 protein fragment containing 107-377
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX Sequence 271 AA;

Query Match 100.0%; Score 669; DB 4; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.1e-68;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVSYGKDPVQHRPMLER 60
 DB 143 IACIGPPNICLDRLNWNITSLAESQLQTRQIKKLEELQKVSYGKDPVQHRPMLER 202

QY 61 IVELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
 DB 203 IVELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 262

QY 121 DKDSGDVAA 129
 DB 263 DKDSGDVAA 271

RESULT 5
 AAE22055
 ID AAE22055 standard; protein; 720 AA.
 XX AAE22055;
 XX 25-JUL-2002 (first entry)
 XX Human Stat3beta protein.
 XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polyompositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion; Statbeta.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 713..714
 FT /note= "Encoded by ACA CCA TTC"
 XX WO200220032-A1.
 XX 14-MAR-2002.
 XX 10-SEP-2001; 2001WO-US028254.
 XX 08-SEP-2000; 2000US-0231212P.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX (UYSF-) UNIV SOUTH FLORIDA.
 XX Yu H, Pardoll D, Jove R, Dalton W;
 XX WPI; 2002-362218/39.
 XX N-PSDB; AAD35066.
 XX Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.
 XX Disclosure; Page 87-89; 94pp; English.
 XX The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing


```

PR 08-SEP-2000; 2000US-0231212P.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
PA (UYSF-) UNIV SOUTH FLORIDA.
XX
PI Yu H, Pardoll D, Jove R, Dalton W;
XX
DR WPI; 2002-362218/39.
DR N-PSDB; AAD35065.
XX
PT Modulating angiogenesis and an immune response in an individual, for
PT treating a hypoxic or ischemic condition, comprises administering a
PT compound that modulates the activity of a signal transducer and activator
PT of transcription 3.
XX
PS Disclosure; Page 83-85; 94pp; English.
XX
XX The invention relates to a method of modulating angiogenesis and immune
XX response. Method involves administering to an individual a compound that
XX modulate the activity of signal transducer and activator of transcription
XX 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
XX hypoxic or ischemic condition or disorder which is the result of stroke,
XX ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
XX tissue ischaemia in the lower extremities, infarction, trauma, vascular
XX occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
XX chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
XX epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
XX nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
XX with neovascularisation. Suppressing an immune response is useful for
XX ameliorating a symptom of an autoimmune disease such as systemic lupus
XX erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
XX Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
XX mixed connective tissue disease, primary biliary cirrhosis, pernicious
XX anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
XX gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
XX idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
XX disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
XX infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
XX dense deposit disease. The method is useful in preventing or treating
XX specific proliferative and oncogenic disease which includes sarcomas and
XX carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
XX fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
XX hypoproliferative disorders, physical trauma, lesions and wounds. The
XX method is also used in gene therapy. The present sequence is human Stat3
XX protein
XX
XX Sequence 769 AA;
XX
Query Match 100.0%; Score 669; DB 5; Length 769;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQQLKLEELQOKYSYKGDPIVQHRPMLER 60
Dd |||||
Dd 249 IACIGPPNICLDRLENWITSLAESQLQTRQQLKLEELQOKYSYKGDPIVQHRPMLER 308
QY 61 IVELFNLKMSAFVVERQCPMPHDPRLPVIKTGVOFTTKVRLLVKFPPELVOLKIKVCI 120
Dd |||||
Dd 309 IVELFNLKMSAFVVERQCPMPHDPRLPVIKTGVOFTTKVRLLVKFPPELVOLKIKVCI 368
QY 121 DKDSGDVAA 129
Dd |||||
Dd 369 DKDSGDVAA 377

RESULT 8
AAE22056
ID AAE22056 standard; protein; 769 AA.
XX
AC AAE22056;
XX
XX 25-JUL-2002 (first entry)
XX

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DE Human protein related to angiogenesis regulation.
XX
XX Human; signal transducer and activator of transcription 3; ischaemia;
XX immune response; Stat3; coronary atherosclerosis; vascular occlusion;
XX hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
XX inflammation; chronic obstructive pulmonary disease; cardiac arrest;
XX insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
XX shock; chronic active hepatitis; adult respiratory distress syndrome;
XX nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
XX Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
XX polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
XX proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
XX carcinoma; degenerative disorder; gene therapy; growth deficiency;
XX cirrhosis; hypoproliferative disorder; lesion.
XX
OS Homo sapiens.
XX
XX WO200220032-A1.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028254.
XX
XX 08-SEP-2000; 2000US-0231212P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX (UYSF-) UNIV SOUTH FLORIDA.
XX
XX Yu H, Pardoll D, Jove R, Dalton W;
XX
XX WPI; 2002-362218/39.
XX
XX Modulating angiogenesis and an immune response in an individual, for
XX treating a hypoxic or ischemic condition, comprises administering a
XX compound that modulates the activity of a signal transducer and activator
XX of transcription 3.
XX
XX Disclosure; Page 83-85; 94pp; English.
XX
XX The invention relates to a method of modulating angiogenesis and immune
XX response. Method involves administering to an individual a compound that
XX modulate the activity of signal transducer and activator of transcription
XX 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
XX hypoxic or ischaemic condition or disorder which is the result of stroke,
XX ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
XX tissue ischaemia in the lower extremities, infarction, trauma, vascular
XX occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
XX chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
XX epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
XX nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
XX with neovascularisation. Suppressing an immune response is useful for
XX ameliorating a symptom of an autoimmune disease such as systemic lupus
XX erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
XX Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
XX mixed connective tissue disease, primary biliary cirrhosis, pernicious
XX anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
XX gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
XX idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
XX disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
XX infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
XX dense deposit disease. The method is useful in preventing or treating
XX specific proliferative and oncogenic disease which includes sarcomas and
XX carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
XX fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
XX hypoproliferative disorders, physical trauma, lesions and wounds. The
XX method is also used in gene therapy. The present sequence is human
XX protein related to angiogenesis regulation
XX
XX Sequence 769 AA;
XX
Query Match 100.0%; Score 669; DB 5; Length 769;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 60
 DB 249 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 308
 QY 61 IVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 120
 DB 309 IVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129
 DB 369 DKDSGDVAA 377
 RESULT 9
 AAR72082
 ID AAR72082 standard; protein; 770 AA.
 XX AC AAR72082;
 XX 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX KW Mouse Stat3 (19sf6).
 DE
 XX KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
 KW receptor recognition factor; transcription factor; cellular debilitation;
 KW derangement; dysfunction; interferon-gamma.
 XX OS Mus sp.
 XX W09508629-A1.
 XX 30-MAR-1995.
 XX 26-SEP-1994; 94WO-US010849.
 XX 24-SEP-1993; 93US-00126588.
 PR 24-SEP-1993; 93US-00126595.
 PR 11-MAR-1994; 94US-00212184.
 PR 11-MAR-1994; 94US-00212185.
 XX (UVRQ) UNIV ROCKEFELLER.
 PA Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 PI WPI; 1995-139598/18.
 DR N-PSDB; AAQ89340.
 XX Receptor recognition factor implicated in transcriptional stimulation of
 PT genes - useful in drug screening assays and/or for treating cellular
 PT debilitations, derangements and/or dysfunctions, etc.
 XX Claim 1; Page 107-110; 160pp; English.
 XX A fragment encoding the human Stat91 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
 CC (Stat1) that was responsive to interferon-gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC and 40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed
 CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct FN field.)
 XX Sequence 770 AA;
 Query Match 100.0%; Score 669; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4.6e-68;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 60
 DB 249 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 308
 QY 61 IVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 120
 DB 309 IVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129
 DB 369 DKDSGDVAA 377

DB 249 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 308
 QY 61 IVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 120
 DB 309 IVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129
 DB 369 DKDSGDVAA 377
 RESULT 10
 AAR82995
 ID AAR82995 standard; protein; 770 AA.
 XX AC AAR82995;
 XX 25-MAR-1996 (first entry)
 DT
 XX DE Mouse liver acute phase response factor.
 XX KW Mouse; acute phase response factor; transcription factor; interleukin-6;
 KW signal transmission; liver; antibody; antisense; ribozyme;
 KW antinflammatory; antitumor; hypotensive; therapy.
 XX OS Mus musculus.
 XX EP676469-A2.
 XX 11-OCT-1995.
 XX 29-MAR-1995; 95EP-00104670.
 PR 04-APR-1994; 94JP-00065825.
 XX (KISH/) KISHIMOTO T.
 PA Akira S, Kishimoto T;
 PI WPI; 1995-346089/45.
 DR N-PSDB; AAT05619.
 XX New acute phase response factor - for developing inhibitory agents for
 PT treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
 PT diseases.
 XX Claim 10; Page 20-22; 31pp; English.
 XX The sequence represents a mouse acute phase response factor (APRF), a
 CC transcription factor related to signal transduction of interleukin-6 (IL-
 CC 6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
 CC library using a polymerase chain reaction product (amplified using
 CC primers derived from an IL-6-treated mouse liver peptide) as a probe.
 CC APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
 CC ribozymes, may be used to treat diseases induced by IL-6, e.g.
 CC inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
 CC hypertension, etc
 XX Sequence 770 AA;
 Query Match 100.0%; Score 669; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4.6e-68;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 60
 DB 249 IACIGGPPNICLDRLNWNITSLAESQLQTRQIKKLELOQKVSXKGDPIVQHRPMLER 308
 QY 61 IVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 120
 DB 309 IVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGQVFTTKVRLLVKFPPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129


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Db          369 DKDSGDVAA 377
|||||
RESULT 11
AAW03176
ID AAW03176 standard; protein; 770 AA.
XX
AC AAW03176;
XX
DT 24-OCT-1996 (first entry)
XX
DE Mouse STAT4.
XX
KW STAT; STAT4; signal transducer and activator of transcription;
KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
KW autoimmune disease; antagonist; therapy.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Domain 398..508
FT /label= DNA binding domain
FT /note= "Claim 3, page 110"
XX
PN WO9620954-A2.
XX
PD 11-JUL-1996.
XX
PF 28-DEC-1995; 95WO-US017025.
XX
PR 06-JAN-1995; 95US-00369796.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI Darnell JE, Wen Z, Horvath CM, Zhong Z;
XX
DR WPI; 1996-333941/33.
DR N-PSDB; AAT31280.
XX
New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,
PT preventing or treating cellular dysfunction, e.g. oncogenesis,
PT inflammation, parasitic disease or autoimmunity.
XX
PS Disclosure; Page 87-90; 138pp; English.
XX
CC Mouse signal transducer and activator of transcription (STAT) protein
CC STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from
CC ligand-activated receptor kinase complexes followed by nuclear
CC translocation and DNA binding to activate transcription. Recombinant
CC STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from
CC splenic/thymic cells. STAT4 includes a DNA-binding domain (see also
CC AAW03167) capable of both receptor recognition and message delivery via
CC DNA binding in a receptor-ligand specific manner. STAT proteins and their
CC DNA binding domains (see also AAW03165-75) are useful for screening
CC antagonists used to inhibit STAT-mediated signal transduction and
CC activation of transcription
XX
SQ Sequence 770 AA;
Query Match 100.0%; Score 669; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQVSYKGDPIVQHRPMLER 60
DB 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKSAFVVERQCPMPHDPRLVITKGVQFTTKVRLLVKFPPELNLQKIKVCI 120
DB 309 IVELFRNLKSAFVVERQCPMPHDPRLVITKGVQFTTKVRLLVKFPPELNLQKIKVCI 368
QY 121 DKDSGDVAA 129

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Db          369 DKDSGDVAA 377
|||||
RESULT 12
AAY03768
ID AAY03768 standard; protein; 770 AA.
XX
AC AAY03768;
XX
DT 11-JUN-1999 (first entry)
XX
DE Human STAT3 allelic variant.
XX
KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;
KW intracellular transcription factor; interleukin-6; medicament; variant;
KW pharmaceutical; autoimmune disease; inflammatory; human.
XX
OS Homo sapiens.
XX
FN EP905234-A2.
XX
PD 31-MAR-1999.
XX
PF 18-FEB-1998; 98EP-00102774.
XX
PR 16-SEP-1997; 97EP-00116061.
XX
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Serlupi-Crescenzi O, Della Pietra L;
XX
DR WPI; 1999-192664/17.
DR N-PSDB; AAX29281.
XX
New human Signal Transducer and Activator of Transcription 3 (STAT3)
PT allelic variant useful for treatment of autoimmune and inflammatory
PT disease.
XX
Claim 2; Page 9-13; 32pp; English.
XX
CC The present sequence represents a predominant allelic variant of human
CC Signal Transducer and Activator of Transcription 3 (STAT3) protein, an
CC intracellular transcription factor which mediates IL-6 signals. The
CC encoding sequence differs from the original published human STAT3 gene
CC sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3
CC DNA molecule can be used for the recombinant expression of the variant.
CC STAT3 protein is useful as a medicament or pharmaceutical composition for
CC treatment of autoimmune or inflammatory diseases
XX
SQ Sequence 770 AA;
Query Match 100.0%; Score 669; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQVSYKGDPIVQHRPMLER 60
DB 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKSAFVVERQCPMPHDPRLVITKGVQFTTKVRLLVKFPPELNLQKIKVCI 120
DB 309 IVELFRNLKSAFVVERQCPMPHDPRLVITKGVQFTTKVRLLVKFPPELNLQKIKVCI 368
QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377
RESULT 13
AAB12377
ID AAB12377 standard; peptide; 770 AA.
XX

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AC AAB12377;
XX 08-NOV-2000 (first entry)
XX N-terminal domain of murine STAT-3 protein.
DE STAT; signal transducer and activator of transcription; crystal;
KW drug design; murine.
XX
XX Mus sp.
FH Key Location/Qualifiers
FT Region 4..9 /label= Alpha helix 1
FT Region 12..21 /label= Alpha helix 2
FT Region 19..21 /label= Alpha helix 2
FT Region 28..33 /label= 3(10) helix of alpha helix 2
FT Region 35..40 /label= Alpha helix 3
FT Region 43..47 /label= Alpha helix 4
FT Region 50..73 /label= Alpha helix 5
FT Region 77..96 /label= Alpha helix 6
FT Region 99..119 /label= Alpha helix 7
FT Region /label= Alpha helix 8
XX
XX US6087478-A.
XX
XX 11-JUL-2000.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX
XX WPI; 2000-505108/45.
XX
XX New crystals of an N-terminal fragment of a signal transducer and
XX activator of transcription that effectively diffracts x-rays, useful for
XX drug screening and development.
XX
XX Disclosure; Fig 1; 42pp; English.
XX
XX The present invention relates to a crystal of an N-terminal fragment of a
XX signal transducer and activator of transcription (STAT) protein. The
XX crystal effectively diffracts x-rays, allowing the determination of the
XX atomic coordinates of the N-terminal domain to a resolution of greater
XX than 5.0 Angstroms. The present sequence is the N-terminal domain of the
XX murine STAT3 protein. The N-terminal domain enables STAT dimers to
XX interact and bind DNA cooperatively, a mechanism important for gene
XX activation. The crystals are useful in drug screening and development by
XX selecting a potential drug by performing rational drug design with the 3-
XX dimensional structure determined for the crystal
XX
XX Sequence 770 AA;
XX
XX Query Match 100.0%; Score 669; DB 3; Length 770;
XX Best Local Similarity 100.0%; Pred. No. 4.6e-68;
XX Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 IACIGGPNICLDLENWITSLSAESQIQTRQIIKKLELOQKVSYGDPVQHRPMLER 60
XX
XX 249 IACIGGPNICLDLENWITSLSAESQIQTRQIIKKLELOQKVSYGDPVQHRPMLER 308
XX
XX 61 IVELFRNLMSAFVVERQPCMPHDPRLPLVKTGQFTTKVRLLVKFPPELNYQLKIKVCI 120
XX
XX Db
XX Qy
XX
XX 309 IVELFRNLMSAFVVERQPCMPHDPRLPLVKTGQFTTKVRLLVKFPPELNYQLKIKVCI 368
XX
XX 121 DKDSGDVAA 129
XX
XX 369 DKDSGDVAA 377
XX
XX
XX RESULT 14
XX AAE14652
XX ID AAE14652 standard; protein; 770 AA.
XX
XX AC AAE14652;
XX
XX 16-JUL-2002 (first entry)
XX
XX Murine STAT3 protein.
XX
XX Signal transducer and activator of transcription; STAT3;
XX drug development; drug discovery; crystal; inflammation; allergy; asthma;
XX leukaemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity;
XX viral disease; growth retardation; murine.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX FT Domain 1..130
XX FT /note= "Conserved N-terminal domain of the STAT family"
XX
XX US6312887-B1.
XX
XX 06-NOV-2001.
XX
XX 24-APR-2000; 2000US-00556273.
XX
XX 23-JAN-1998; 98US-00012710.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX
XX WPI; 2002-033337/04.
XX
XX Identifying compounds that bind to signal transducer and activator of
XX transcription proteins, useful for the production of new drugs.
XX
XX Example; Col 47-50; 44pp; English.
XX
XX The invention relates to methods for detecting compounds that bind to
XX signal transducer and activator of transcription (STAT) proteins for the
XX discovery and development of new drug compounds based on the structural
XX properties of the protein crystal. The methods include: identifying a
XX compound that binds to the N-terminal domain of a STAT protein,
XX identifying a compound that enhances or diminishes the binding of the
XX dimeric STAT proteins to each other and/or their nucleic acid binding
XX site; or identifying a compound that enhances or diminishes the ability
XX of STAT protein dimers to induce the expression of a gene operably under
XX the control of a promoter containing at least two adjacent weak binding
XX sites for STAT protein dimers. The methods are used for identifying new
XX drugs. An antagonist of STAT N-terminal dimeric interactions that
XX inhibits the binding of the STAT dimers to adjacent weak binding sites on
XX a promoter of a gene, could be useful as drugs in the treatment of
XX diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other
XX hand, an agonist of N-terminal dimeric interactions between STAT dimers,
XX can be used as drugs in the treatment of diseases e.g. anaemia,
XX neutropaenia, thrombocytopaenia, cancer, obesity, viral diseases and
XX growth retardation. The present sequence is murine STAT3 protein
XX
XX SQ Sequence 770 AA;
XX
XX Query Match 100.0%; Score 669; DB 5; Length 770;
XX Best Local Similarity 100.0%; Pred. No. 4.6e-68;
XX Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1	IACIGGPNICLDRLNNITSLAESQLOTRQOIKLEELQOKVSKYGGDPVOHRPMLER	60
Db	249	IACIGGPNICLDRLNNITSLAESQLOTRQOIKLEELQOKVSKYGGDPVOHRPMLER	308
Qy	61	IVELFRNLMSAFVVERQPCMPMHDPRLVKTGVQFTTKVRLLVKFPPELNTQLKIKVCI	120
Db	309	IVELFRNLMSAFVVERQPCMPMHDPRLVKTGVQFTTKVRLLVKFPPELNTQLKIKVCI	368
Qy	121	DKDSGDVAA	129
Db	369	DKDSGDVAA	377

RESULT 15

ABG69497
ID ABG69497 standard; protein; 770 AA.

AC ABG69497;

DT 21-OCT-2002 (first entry)

Human bait protein STAT3.

Human; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;
non-insulin diabetes mellitus; obesity; selected interacting domain; SID;
protein-protein interaction map; PIM; anorectic; metabolic disorder.

OS Homo sapiens.

PN WO200253726-A2.

11-JUL-2002.

28-DEC-2001; 2001WO-EP015423.

PR 02-JAN-2001; 2001US-0259377P.

PA (HYBR-) HYBRIGENICS.

PA (CNRS) CENT NAT RECH SCI.

PI Legrain P, Marullo S, Jockers R;

DR WPI; 2002-583612/62.

DR N-PSDB; ABS51033.

Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders.

PS Claim 1; Page 54; 125pp; English.

The invention relates to a complex of protein-protein interactions (forming a protein-protein interaction map, PIM) in adipocyte cells as defined in the specification, or polynucleotides in adipocytes encoding the for polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by culturing a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the expression of which is toxic for the recombinant host cell which is expressed with two vectors, a first hybrid polypeptide and DNA binding domain polynucleotide encoding a first hybrid polypeptide and DNA binding domain and the second vector comprising a polynucleotide encoding a second hybrid polypeptide and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the growth of the recombinant host cell (i.e. using the yeast two-hybrid system). The complexes are useful for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The compound isolated by the method is useful for treating and preventing obesity or metabolic diseases. The interactions between the proteins of the complex further define a set of selected interacting domains, SID.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 16.141 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-24
Perfect score: 669
Sequence: 1 IACIGPPNICLDRLNENWIT.....LNYQLKIKVICDKSGDVAA 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	669	100.0	129	3	US-09-387-418A-24
2	669	100.0	185	3	US-09-387-418A-23
3	669	100.0	223	3	US-09-387-418A-22
4	669	100.0	271	3	US-09-387-418A-9
5	669	100.0	770	1	US-08-369-796-12
6	669	100.0	770	1	US-08-416-581B-9
7	669	100.0	770	2	US-08-852-091-12
8	669	100.0	770	2	US-08-820-754-12
9	669	100.0	770	3	US-08-956-652-12
10	669	100.0	770	3	US-08-956-869-12
11	669	100.0	770	3	US-09-012-710-8
12	669	100.0	770	3	US-08-948-547-12
13	669	100.0	770	3	US-09-364-970-3
14	669	100.0	770	3	US-09-364-970-5
15	669	100.0	770	3	US-09-556-273-8
16	669	100.0	770	3	US-08-956-653A-12
17	669	100.0	770	3	US-09-526-542-2
18	669	100.0	770	4	US-08-212-185-12
19	669	100.0	770	4	US-10-117-087-2
20	669	100.0	770	5	PCT-US95-17025-12
21	664	99.3	770	1	US-08-416-581B-1
22	664	99.3	770	1	US-08-416-581B-5
23	664	99.3	770	3	US-09-087-465-6
24	664	99.3	770	4	US-09-972-800A-6
25	664	99.3	771	1	US-08-276-099A-14
26	664	99.3	771	1	US-08-781-890-14
27	571	85.4	229	3	US-09-387-418A-18

28	571	85.4	229	3	US-09-387-418A-28	Sequence 28, Appl
29	571	85.4	229	3	US-09-387-418A-30	Sequence 30, Appl
30	571	85.4	229	3	US-09-387-418A-31	Sequence 31, Appl
31	571	85.4	229	3	US-09-387-418A-14	Sequence 14, Appl
32	554	82.8	229	3	US-09-387-418A-29	Sequence 29, Appl
33	494	73.8	96	3	US-09-387-418A-25	Sequence 25, Appl
34	493	73.7	213	3	US-09-387-418A-19	Sequence 19, Appl
35	493	73.7	236	3	US-09-387-418A-15	Sequence 15, Appl
36	436	65.2	268	3	US-09-387-418A-12	Sequence 12, Appl
37	436	65.2	582	4	US-09-430-806A-3	Sequence 3, Appl
38	436	65.2	712	1	US-08-369-796-6	Sequence 6, Appl
39	436	65.2	712	2	US-08-852-091-6	Sequence 6, Appl
40	436	65.2	712	2	US-08-820-754-6	Sequence 6, Appl
41	436	65.2	712	3	US-08-956-652-6	Sequence 6, Appl
42	436	65.2	712	3	US-08-956-869-6	Sequence 6, Appl
43	436	65.2	712	3	US-08-948-547-6	Sequence 6, Appl
44	436	65.2	712	3	US-08-956-653A-6	Sequence 6, Appl
45	436	65.2	712	4	US-08-212-185-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-387-418A-24
; Sequence 24, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-24

Query Match	100.0%	Score 669;	DB 3;	Length 129;
Best Local Similarity	100.0%	Pred. No. 5.5e-69;	Mismatches 0;	Indels 0;
Matches 129;	Conservative 0;			Gaps 0;
QY	1	IACIGPPNICLDRLNENWITSLAESQLQTRQIKKLEELQKQKVSYGDPVQHRPML	60	
Db	1	IACIGPPNICLDRLNENWITSLAESQLQTRQIKKLEELQKQKVSYGDPVQHRPML	60	
QY	61	IVELFRLMKSAFVVERQPCMPHDPRLVITGVQFTTKVRLLVKFPPELNYQLKVICI	120	
Db	61	IVELFRLMKSAFVVERQPCMPHDPRLVITGVQFTTKVRLLVKFPPELNYQLKVICI	120	
QY	121	DKDSDGVAA	129	
Db	121	DKDSDGVAA	129	
RESULT 2				
US-09-387-418A-23				
; Sequence 23, Application US/09387418A				
; Patent No. 6391572				
; GENERAL INFORMATION:				
; APPLICANT: Zhang, Xiaokui				
; APPLICANT: Wrzeszczynska, Melissa H				
; APPLICANT: Horvath, Curt M				
; APPLICANT: Darnell Jr., James E				
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR				
; TITLE OF INVENTION: INTERACTIONS				

; FILE REFERENCE: 600-1-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-23

Query Match 100.0%; Score 669; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 8.9e-69;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIQKLEELQOKVSYKGDPIVQHRPMLER 60
DB 57 IACIGPPNICLDRLNWTSLAESQLQTRQIQKLEELQOKVSYKGDPIVQHRPMLER 116
QY 61 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
DB 117 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 176

QY 121 DKDSGDVAA 129
DB 177 DKDSGDVAA 185

RESULT 3
US-09-387-418A-22
; Sequence 22, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-22

Query Match 100.0%; Score 669; DB 3; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.1e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIQKLEELQOKVSYKGDPIVQHRPMLER 60
DB 95 IACIGPPNICLDRLNWTSLAESQLQTRQIQKLEELQOKVSYKGDPIVQHRPMLER 154
QY 61 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
DB 155 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 214

QY 121 DKDSGDVAA 129
DB 215 DKDSGDVAA 223

RESULT 4
US-09-387-418A-9
; Sequence 9, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-9

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Best Local Similarity 100.0%; Pred. No. 1.5e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
DB 203 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 262

QY 121 DKDSGDVAA 129
DB 263 DKDSGDVAA 271

RESULT 5
US-08-369-796-12
; Sequence 12, Application US/08369796
; Patent No. 5711622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-369-796-12

Query Match 100.0%; Score 669; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308

QY 61 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
DB 309 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377

RESULT 6
US-08-416-581B-9
Sequence 9, Application US/08416581B
Patent No. 5719042
GENERAL INFORMATION:
APPLICANT: Kishimoto, Tadimitsu
APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-5825/1994
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-37891
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-416-581B-9

Query Match 100.0%; Score 669; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
DB 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308

QY 61 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120

DB 309 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377

RESULT 7
US-08-852-091-12
Sequence 12, Application US/08852091
Patent No. 5883228
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-091-12

Query Match 100.0%; Score 669; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308

QY 61 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
DB 309 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377

RESULT 8

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US-08-820-754-12
; Sequence 12, Application US/08820754
; Patent No. 5976835
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,754
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-820-754-12

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Qy 121 DKDSGDVAA 129
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US-08-956-652-12
; Sequence 12, Application US/08956652
; Patent No. 6013475
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
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; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-956-652-12

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Qy 121 DKDSGDVAA 129
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QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 10

US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
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; FILING DATE:
; CLASSIFICATION:
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; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12
Query Match 100.0%; Score 669; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 309 IVELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

RESULT 12

US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118

QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377
RESULT 11
US-09-012-710-8
; Sequence 8, Application US/09012710
; Patent No. 6087478
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-012-710-8

Query Match 100.0%; Score 669; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6e-68;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; FILING DATE:
; CLASSIFICATION:
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; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US/07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-948-547-12

Query Match 100.0%; Score 669; DB 3; Length 770;
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US-09-364-970-3
; Sequence 3, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT APPLICATION NUMBER: US/09/364,970
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-364-970-3

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DB 249 IACIGGPPNICLDRLNNWITSLAESOLQTRQOIKKLEELQKQVSYKGDPIVQHRPMLER 308
QY 61 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
DB 309 IVELFRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377

RESULT 14

US-09-364-970-5
; Sequence 5, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
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; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
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 ; Patent No. 6312887
 ; GENERAL INFORMATION:
 ; APPLICANT: Vinkemeier, Uwe
 ; APPLICANT: Moarefi, Ismail
 ; APPLICANT: Darnell, Jr., James E.
 ; APPLICANT: Kurlyan, John
 ; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
 ; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue, 4th Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
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 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/556,273
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/012,710
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-194
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; US-09-556-273-8

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QM protein - protein search, using sw model

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	669	100.0	185	13 US-10-090-185-23	Sequence 23, Appl
3	669	100.0	223	13 US-10-090-185-22	Sequence 22, Appl
4	669	100.0	271	13 US-10-090-185-9	Sequence 9, Appli
5	669	100.0	720	15 US-10-380-020-4	Sequence 4, Appli
6	669	100.0	769	15 US-10-380-020-2	Sequence 2, Appli
7	669	100.0	769	15 US-10-380-020-5	Sequence 5, Appli
8	669	100.0	770	11 US-09-876-773-12	Sequence 12, Appl
9	669	100.0	770	14 US-10-045-792-8	Sequence 8, Appli
10	669	100.0	770	14 US-10-038-010-56	Sequence 56, Appl
11	669	100.0	770	14 US-10-117-087-2	Sequence 2, Appli
12	669	100.0	770	17 US-10-639-617-12	Sequence 12, Appl
13	669	100.0	793	9 US-09-925-302-780	Sequence 780, App

14	669	100.0	793	10 US-09-925-302-780	Sequence 780, App
15	666	99.6	770	15 US-10-116-275-329	Sequence 329, App
16	664	99.3	770	15 US-10-116-275-349	Sequence 349, App
17	571	85.4	229	13 US-10-090-185-18	Sequence 18, Appl
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19	571	85.4	229	13 US-10-090-185-30	Sequence 30, Appl
20	571	85.4	229	13 US-10-090-185-31	Sequence 31, Appl
21	571	85.4	252	13 US-10-090-185-14	Sequence 14, Appl
22	554	82.8	229	13 US-10-090-185-29	Sequence 29, Appl
23	494	73.8	96	13 US-10-090-185-25	Sequence 25, Appl
24	493	73.7	213	13 US-10-090-185-19	Sequence 19, Appl
25	493	73.7	236	13 US-10-090-185-15	Sequence 15, Appl
26	436	65.2	268	13 US-10-090-185-12	Sequence 12, Appl
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28	436	65.2	712	11 US-09-876-773-6	Sequence 6, Appli
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31	436	65.2	712	17 US-10-936-390-5	Sequence 5, Appli
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35	436	65.2	750	14 US-10-308-279-44	Sequence 44, Appl
36	436	65.2	750	16 US-10-755-889-352	Sequence 352, App
37	436	65.2	750	16 US-10-755-889-823	Sequence 823, App
38	436	65.2	750	17 US-10-492-043-19	Sequence 19, Appl
39	436	65.2	750	17 US-10-639-617-4	Sequence 4, Appli
40	436	65.2	786	9 US-09-925-297-550	Sequence 550, App
41	432	64.6	749	9 US-09-833-205-4	Sequence 4, Appli
42	395	59.0	749	9 US-09-833-205-6	Sequence 6, Appli
43	395	59.0	749	11 US-09-876-773-8	Sequence 8, Appli
44	395	59.0	749	14 US-10-045-792-7	Sequence 7, Appli
45	395	59.0	749	14 US-10-205-194-39	Sequence 39, Appli

ALIGNMENTS

RESULT 1
US-10-090-185-24
; Sequence 24, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melisea H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-24

Query Match 100.0%; Score 669; DB 13; Length 129;
Best Local Similarity 100.0%; Pred. No. 9.6e-67;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
DB 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
QY 61 IVELFRLMKSAFVVERQCPMPHDPRLVIKTVQFTTKVRLLVKFPPELNYQLKIKVCI 120
DB 61 IVELFRLMKSAFVVERQCPMPHDPRLVIKTVQFTTKVRLLVKFPPELNYQLKIKVCI 120

QY 121 DKDSGDVAA 129
| | | | |
Db 121 DKDSGDVAA 129
| | | | |
RESULT 2
US-10-090-185-23
; Sequence 23, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-23
Query Match 100.0%; Score 669; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.5e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSXKGDPIVQHRPMLER 60
| | | | |
Db 57 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSXKGDPIVQHRPMLER 116
| | | | |
QY 61 IVELFRLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
| | | | |
Db 117 IVELFRLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 176
| | | | |
QY 121 DKDSGDVAA 129
| | | | |
Db 177 DKDSGDVAA 185
| | | | |
RESULT 3
US-10-090-185-22
; Sequence 22, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 22
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-22
Query Match 100.0%; Score 669; DB 13; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.9e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSXKGDPIVQHRPMLER 60
| | | | |
Db 95 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSXKGDPIVQHRPMLER 154
| | | | |
QY 61 IVELFRLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
| | | | |
Db 155 IVELFRLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 214
| | | | |
QY 121 DKDSGDVAA 129
| | | | |
Db 215 DKDSGDVAA 223
| | | | |
RESULT 4
US-10-090-185-9
; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-9
Query Match 100.0%; Score 669; DB 13; Length 271;
Best Local Similarity 100.0%; Pred. No. 2.5e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSXKGDPIVQHRPMLER 60
| | | | |
Db 143 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSXKGDPIVQHRPMLER 202
| | | | |
QY 61 IVELFRLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
| | | | |
Db 203 IVELFRLMKSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 262
| | | | |
QY 121 DKDSGDVAA 129
| | | | |
Db 263 DKDSGDVAA 271
| | | | |
RESULT 5
US-10-380-020-4
; Sequence 4, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 4

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; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-4

Query Match      100.0%; Score 669; DB 15; Length 720;
Best Local Similarity 100.0%; Pred. No. 8.8e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60
DB 249 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
DB 309 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377

RESULT 6
US-10-380-020-2
; Sequence 2, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 769
; TYPE: PRT<
; ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match      100.0%; Score 669; DB 15; Length 769;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60
DB 249 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
DB 309 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377

RESULT 7
US-10-380-020-5
; Sequence 5, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999

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; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-5

Query Match      100.0%; Score 669; DB 15; Length 769;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60
DB 249 IACIGPPNICLDRLENWITSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 120
DB 309 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
DB 369 DKDSGDVAA 377

RESULT 8
US-09-876-773-12
; Sequence 12, Application US/09876773
; Publication No. US20040058318A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Fu, Xian-Yuan
; Schindler, Christian W.
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/876,773
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP

```

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match 100.0%; Score 669; DB 11; Length 770;

Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60

Db 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 308

QY 61 IVELFNLKMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKFPPELNYQLKIKVCI 120

Db 309 IVELFNLKMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129

Db 369 DKDSGDVAA 377

RESULT 9

US-10-045-792-8

; Sequence 8, Application US/10045792

; Publication No. US20030003563A1

GENERAL INFORMATION:

APPLICANT: Vinkemeier, Uwe
Moarefi, Iemal
Darnell, Jr., James E.
Kurlyan, John

TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPL APPLICATION NUMBER: US/10/045,792

FILING DATE: 19-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/012,710

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-194

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-045-792-8

Query Match 100.0%; Score 669; DB 14; Length 770;

Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60

Db 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 308

QY 61 IVELFNLKMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKFPPELNYQLKIKVCI 120

Db 309 IVELFNLKMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129

Db 369 DKDSGDVAA 377

RESULT 10

US-10-038-010-56

; Sequence 56, Application US/10038010

; Publication No. US20030040089A1

GENERAL INFORMATION:

APPLICANT: HYBRIGENICS

APPLICANT: Pierre, Legrain

TITLE OF INVENTION: Protein-protein interactions in adipocyte cells

FILE REFERENCE: B4767A

CURRENT APPLICATION NUMBER: US/10/038,010

CURRENT FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US 60/259,377

PRIOR FILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patent in version 3.1

SEQ ID NO 56

LENGTH: 770

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: STAT3 : Transcription factor

LOCATION: (1)-(770)

OTHER INFORMATION:

US-10-038-010-56

Query Match 100.0%; Score 669; DB 14; Length 770;

Best Local Similarity 100.0%; Pred. No. 9.6e-66;

Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 60

Db 249 IACIGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKQVSYKGDPIVQHRPMLER 308

QY 61 IVELFNLKMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKFPPELNYQLKIKVCI 120

Db 309 IVELFNLKMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKFPPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129

Db 369 DKDSGDVAA 377

RESULT 11

US-10-117-087-2

; Sequence 2, Application US/10117087

; Publication No. US20030166854A1

GENERAL INFORMATION:

APPLICANT: SERLUPI-CRESCENZI, Ottaviano

APPLICANT: DELLA PIETRA, Linda

;; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
;; FILE REFERENCE: SERLUIP-2
;; CURRENT APPLICATION NUMBER: US/10/117,087
;; CURRENT FILING DATE: 2002-04-08
;; PRIOR APPLICATION NUMBER: US/09/526,542
;; PRIOR FILING DATE: 2000-03-19
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: Patent in version 3.0
;; SEQ ID NO 2
;; LENGTH: 770
;; TYPE: PRT
;; ORGANISM: Human
US-10-117-087-2

Query Match 100.0%; Score 669; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 60
Db 249 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
Db 309 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 12

US-10-639-617-12
;; Sequence 12, Application US/10639617
;; Publication No. US20050079543A1
;; GENERAL INFORMATION:
;; APPLICANT: Darnell Jr., James E.
;; Schindler, Christian W.
;; Fu, Xian-Yuan
;; Wen, Zilong
;; Zhong, Zhong
;; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
;; SEQUENCES AND METHODS OF USE THEREOF
;; NUMBER OF SEQUENCES: 25
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION NUMBER: US/10/639,617
;; FILING DATE: 12-Aug-2003
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/212,185
;; FILING DATE: 11-MAR-1994
;; APPLICATION NUMBER: US 07/980,498
;; FILING DATE: 23-NOV-1992
;; APPLICATION NUMBER: US 07/854,296
;; FILING DATE: 19-MAR-1992
;; APPLICATION NUMBER: WO US93/02569
;; FILING DATE: 19-MAR-1993
;; APPLICATION NUMBER: US 08/126,588
;; FILING DATE: 24-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.

;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 770 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

Query Match 100.0%; Score 669; DB 17; Length 770;
Best Local Similarity 100.0%; Pred. No. 9.6e-66;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 60
Db 249 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
Db 309 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 13

US-09-925-302-780
;; Sequence 780, Application US/09925302
;; Patent No. US20020044941A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;; FILE REFERENCE: PA104
;; CURRENT APPLICATION NUMBER: US/09/925,302
;; CURRENT FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: PCT/US00/05918
;; PRIOR FILING DATE: 2000-03-08
;; PRIOR APPLICATION NUMBER: 60/124,270
;; PRIOR FILING DATE: 1999-03-12
;; NUMBER OF SEQ ID NOS: 896
;; SOFTWARE: Patent in Ver. 2.0
;; SEQ ID NO 780
;; LENGTH: 793
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match 100.0%; Score 669; DB 9; Length 793;
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 60
Db 272 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLEELQKVSYKGDPIVQHRPMLER 331

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
Db 332 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPELNYQLKIKVCI 391

QY 121 DKDSGDVAA 129
Db 392 DKDSGDVAA 400

RESULT 14

US-09-925-302-780

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:24:07 ; Search time 12.1698 Seconds
(without alignments)
1019.898 Million cell updates/sec

Title: US-10-090-185-24
Perfect score: 669
Sequence: 1 IACIGPPNICLDRLNWT.....LNYQKIKVICDKSGDVAA 129
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	669	100.0	770	2 I49508	ISGF3 p91-related
2	664	99.3	770	2 A54444	DNA-binding protei
3	390.5	58.4	739	2 A46159	interferon-depende
4	375	56.1	748	2 A56047	gamma-interferon a
5	257	38.4	851	2 A46160	interferon alpha-1
6	160.5	24.0	786	2 I49274	mammary gland fact
7	160.5	24.0	793	2 S54772	mammary gland fact
8	160.5	24.0	794	2 G02317	transcription acti
9	142	21.2	794	2 S55527	mammary gland fact
10	98	14.6	848	2 A54740	interleukin-4-indu
11	93.5	14.0	837	2 I57557	DNA-Binding Protei
12	80.5	12.0	464	2 H90279	microtubule bindin
13	80	12.0	393	2 T25063	hypothetical prote
14	79	11.8	589	1 NDECAS	type I site-specif
15	78.5	11.7	191	2 B70042	hypothetical prote
16	78.5	11.7	253	2 F84840	hypothetical prote
17	78	11.7	498	2 T06667	argininosuccinate
18	77	11.5	590	2 A48461	ovarian abundan m
19	75.5	11.3	257	2 B96003	probable transcript
20	75.5	11.3	926	2 T39082	hypothetical prote
21	75	11.2	121	2 G90550	hypothetical prote
22	75	11.2	623	2 G81420	hypothetical prote
23	75	11.2	695	2 T39954	probable gtpase ac
24	74.5	11.1	256	2 T48076	60S RIBOSOMAL PROT
25	74.5	11.1	900	2 T14277	myosin-like protei
26	74.5	11.1	2783	1 A41948	alpha-fetoprotein
27	74	11.1	893	2 F72253	hypothetical prote
28	73	10.9	546	2 AC2368	hypothetical prote
29	73	10.9	575	2 AF2374	hypothetical prote

30	72.5	10.8	257	2 T00423	ribosomal protein
31	72.5	10.8	432	2 A85040	hypothetical prote
32	72.5	10.8	447	2 S54631	HST3 protein - yea
33	72.5	10.8	1218	2 T14265	golgin-245 - mouse
34	72.5	10.8	1331	1 XORTDH	xanthine dehydroge
35	72	10.8	335	2 T25110	hypothetical prote
36	72	10.8	346	2 F87844	protein T22Cl.6 [i
37	72	10.8	393	2 S32458	4-hydroxyphenylpyr
38	72	10.8	393	2 S32821	4-hydroxyphenylpyr
39	72	10.8	1999	1 S21801	myosin heavy chain
40	71.5	10.7	217	1 S73360	heat shock protein
41	71.5	10.7	328	2 A93345	conserved hypochet
42	71.5	10.7	573	2 A86253	hypothetical prote
43	71.5	10.7	879	2 F96558	probable protein k
44	71.5	10.7	1529	2 A59310	unconventional myo
45	71.5	10.7	3329	2 T42205	breast cancer susc

ALIGNMENTS

RESULT 1

I49508
ISGF3 p91-related transcription factor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49508; I49009
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr
A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: I49508
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P42227; GB:L29278; NID:G476715; PIDN:AAA37254.1; PID:G47671
R;Raz, R.; Durbin, J.E.; Levy, D.E.
J. Biol. Chem. 269, 24391-24395, 1994
A;Title: Acute phase response factor and additional members of the interferon-stimulate
A;Reference number: I49009; MUID:95014185; PMID:7523373
A;Accession: I49009
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-393,'M',395-700,702-770 <RE2>
A;Cross-references: EMBL:U08378; NID:G473889; PIDN:AAA56668.1; PID:G473890
C;Genetics:
A;Gene: APRF
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match	100.0%;	Score	669;	DB	2;	Length	770;
Best Local Similarity	100.0%;	Pred. No.	1.8e-55;				
Matches	129;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	IACIGPPNICLDRLNWTISLAESQLQTRQIKLEELQKKVSYKSGDPVQHRPMLER	60				
Db	249	IACIGPPNICLDRLNWTISLAESQLQTRQIKLEELQKKVSYKSGDPVQHRPMLER	308				
QY	61	IYELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI	120				
Db	309	IYELFNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI	368				
QY	121	DKDSGDVAA	129				
Db	369	DKDSGDVAA	377				

RESULT 2

A54444
DNA-binding protein APRF - human
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: A54444
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su

Query Match	38.4%	Score 257;	DB 2;	Length 851;
Best Local Similarity	42.6%;	Pred. No. 2.3e-16;		
Matches	52;	Conservative	25;	Mismatches 45;
				Indels 0;
				Gaps 0;

A;Reference number: S54772; MUID:95237198; PMID:7720707
A;Accession: S54772
A;Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A;Residues: 1-793 <MUI>
A;Cross-references: UNIPROT:P42230; UNIPROT:O9JTA0; EMBL:Z48538; NID:g758633; PIDN:CAA
R;Liou, X.; Robinson, G.W.; Guilleux, F.; Groner, B.; Hennighausen, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995
A>Title: Cloning and expression of Stats and an additional homologous (Stat5b) involved
in cytokine signaling
A;Reference number: I49273; MUID:96004632; PMID:7568026
A;Accession: I49273
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-793 <RES>
A;Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972
C;Genetics:
A:Gene: Stat5a
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 24.0%; Score 160.5; DB 2; Length 793;
Best Local Similarity 37.6%; Pred. No. 3e-07;
Matches 38; Conservative 17; Mismatches 37; Indels 9; Gaps 2;

Qy 5 GGPNICLDLENWITS LAESQLTROQIKLEELQOKVSKYKGDPIVQRHMLERIVEL 64
||||| :||| ||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 265 GGPPEGLDVLQSCKEKLAIINWRQQIRAEHLCCQLPTPG-PVEEMLAENVATITDI 323
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 65 FRNLKSAFVVVERPCMPMHDPRLVIKTGVQTFTTKVRLLV 105
|:::| ::||| |:::| ::||| |:::| ::||| |:::| ::||| |:::| ::|||
Db 324 ISALVTTFIIKKP-----PQVLKTQTKFAATVRLLV 356
|:::| ::||| |:::| ::||| |:::| ::||| |:::| ::||| |:::| ::|||

RESULT 8
G02317
transcription activator stat5A - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02317
R;Lin, J.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g1
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 24.0%; Score 160.5; DB 2; Length 794;
Best Local Similarity 37.6%; Pred. No. 3e-07;
Matches 38; Conservative 17; Mismatches 37; Indels 9; Gaps 2;

Qy 5 GGPNICLDLENWITS LAESQLTROQIKLEELQOKVSKYKGDPIVQRHMLERIVEL 64
||||| :||| ||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 265 GGPPEGLDVLQSCKEKLAIINWRQQIRAEHLCCQLPTPG-PVEEMLAENVATITDI 323
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 65 FRNLKSAFVVVERPCMPMHDPRLVIKTGVQTFTTKVRLLV 105
|:::~| ~:||| |:::~| ~:||| |:::~| ~:||| |:::~| ~:||| |:::~| ~:|||
Db 324 ISALVTTFIIKKP-----PQVLKTQTKFAATVRLLV 356
|:::~| ~:||| |:::~| ~:||| |:::~| ~:||| |:::~| ~:||| |:::~| ~:|||

RESULT 9
S55527
mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55527; S44353
R;Wakao, H.; Guillieux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A>Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regul
A;Reference number: S55527; MUID:95188889; PMID:7882987
A;Accession: S55527
A:Molecule type: mRNA

C;Superfamily: 4-hydroxyphenylpyruvate_dioxygenase

Query Match 12.0%; Score 80; DB 2; Length 393;
Best Local Similarity 20.8%; Pred. No. 5.5;
Matches 35; Conservative 23; Mismatches 56; Indels 54; Gaps 6;

QY 3 CIGPPNICLDRLNW-----ITSLAESQLQTRQI-----33
DB 183 CVGNQPLQMSAVOMTEKVLKFRFWSVDDSMIHTYSALRSIVTNFETIKMPINEP 242
QY 34 -----KKLEELQKVSKGDPVIOHRPMLERIVEL-----FRNLKMGAF--VVE 76
DB 243 ATSDKKAIISOIEVDYGGSGVQHIALNTSDIITAEALRARCCEFLSPSSVDYDLKE 302
QY 77 RQCPMPHPRPLVIKTVGFTTKVRLLVKPELNYOLKI--KVICDK 122
DB 303 RLAASSM-----VVKEDMDRLQKLHILVDFDENGYLLOIFSKPCQDR 344

RESULT 14

NDECAS

type I site-specific deoxyribonuclease (RC 3.1.21.3) EcoA chain S - Escherichia coli
N;Alternate names: deoxyribonuclease, EcoA, S chain (ATP- and S-adenosyl-L-methionine-de
C;Species: Escherichia coli
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 30-Jun-1993
C;Accession: A32343
R;Cowan, G.M.; Gann, A.A.F.; Murray, N.E.
Cell 56, 103-109, 1989
A;Title: Conservation of complex DNA recognition domains between families of restriction
A;Reference number: A32343; MUID:89089749; PMID:2642743

A;Accession: A32343

A;Molecule type: DNA

A;Residues: 1-589 <COW>

C;Comment: This S chain, one of three components (S, R, and M chains) of type I, site-spe

cificity for the target sequence, GAG.

C;Superfamily: type I site-specific deoxyribonuclease EcoA chain S

C;Keywords: DNA binding; hydrolase; restriction modification system

Query Match 11.8%; Score 79; DB 1; Length 589;
Best Local Similarity 24.4%; Pred. No. 11;
Matches 31; Conservative 25; Mismatches 41; Indels 30; Gaps 6;

QY 10 ICLDRLENWITSLSAESQLQTRQ-----IKLEELQOKVSYKG-----DPV 51
DB 6 LIVDHMETW-----TSALQTRTAGSGSKIDLYGIKKLELLELAVRGKLVPQDPND 60
QY 52 QHRPMLERIVELFRNLKSAFVVERQPCMP--MHPDRPLVIKTVGFTTKVRLLVKPE 109
DB 61 EPASELLKRIAEBKAELVKQGIKKQKP-LPEISEBEKPELPDGEWTT-----LTRIAE 115
QY 110 LNYOLKI 116
DB 116 INPKIDV 122

RESULT 15

B70042

hypothetical protein yviE - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 03-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: B70042

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, F.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B70042
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-191 <KUN>
A;Cross-references: UNIPROT:P96502; GB:299122; GB:AL009126; NID:g2636029; PIDN:CAB15556
A;Experimental source: strain 168
C;Genetics:
A;Gene: yviE
C;Superfamily: Bacillus subtilis hypothetical protein yviE

Query Match 11.7%; Score 78.5; DB 2; Length 191;
Best Local Similarity 20.9%; Pred. No. 3.3;
Matches 31; Conservative 25; Mismatches 41; Indels 51; Gaps 7;

QY 7 PPNICLDRLNWTSLAESQLQTRQIKLEELQ-----KVS 45
DB 48 PGKLTIDQTAW-----EELDRKHVFKRIEAAQQGHEDVMEGIARTABEGDELMKIEN 101
QY 46 KGDPPIV-QHRPMLERIVELFRNLKS-----AFVVERQPCMPHPRPLV 90
DB 102 KGNPIASQARRNEMHQIQUGENYAFSLSRVKIQYTPSQLDVQITPRKPVIOABPHRPI- 160
QY 91 IKTGVOFT---TKVRLLVKPELNYOLK 115
DB 161 ----VEYTPGNVVDML-QYPDLNIDVE 183

Search completed: May 25, 2005, 17:45:25
Job time : 14.1698 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	669	100.0	163	2	QN145	QN145 macaca mula
2	669	100.0	770	1	STA3_BOVIN	P61635 bos taurus
3	669	100.0	770	1	STA3_HUMAN	P40763 homo sapien
4	669	100.0	770	1	STA3_MOUSE	P42227 mus musculus
5	666	99.6	770	1	STA3_RAT	P52631 rattus norv
6	665	99.4	771	2	Q6DV79	Q6dv79 gallus gall
7	658	98.4	769	2	Q6PVX8	Q6pvx8 xenopus lae
8	650	97.2	766	2	Q7ZXK3	Q7zxk3 xenopus lae
9	637	95.2	414	2	Q7ZTS5	Q7zts5 brachydanio
10	637	95.2	786	2	Q6NV46	Q6nv46 brachydanio
11	637	95.2	806	2	Q93599	Q93599 brachydanio
12	635	94.9	765	2	Q6DVF3	Q6dvf3 oryzias lat
13	635	94.9	785	2	Q6GUE7	Q6gue7 oryzias lat
14	624	93.3	764	2	Q90Y16	Q90y16 tetraodon f
15	600	89.7	767	2	O13133	O13133 oncorhynchu
16	555	83.0	161	2	Q7Q4W5	Q7q4w5 bos taurus
17	446	66.7	751	2	Q6JGNO	Q6jgno xenopus lae
18	436	65.2	750	1	STA1_HUMAN	P42224 homo sapien
19	436	65.2	750	2	Q68D00	Q68d00 homo sapien
20	434	64.9	758	2	Q90Y17	Q90y17 tetraodon f
21	432	64.6	712	2	Q6P6Q7	Q6p6q7 rattus norv
22	432	64.6	749	2	Q9QXK0	Q9qxk0 rattus norv
23	430	64.3	757	2	Q764M5	Q764m5 sus scrofa
24	428	64.0	749	2	Q8C497	Q8c497 mus musculus
25	427	63.8	712	2	Q99K94	Q99k94 mus musculus
26	427	63.8	749	2	Q8C3V4	Q8c3v4 mus musculus
27	427	63.8	749	2	Q9D323	Q9d323 mus musculus
28	427	63.8	755	2	Q8C8M3	Q8c8m3 mus musculus
29	422	63.1	754	2	O13131	O13131 oncorhynchu
30	415	62.0	1153	2	Q8JF55	Q8jfs5 brachydanio
31	410	61.3	754	2	O13132	O13132 oncorhynchu

AC P61635;

DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3.
 GN Name=STAT3;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
 RT "The STAT3B-encoding gene was flipped across the STAT3/STAT5A-locus
 RL during ruminant evolution.";
 CC Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes (By similarity).
 CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation (By similarity).
 CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AJ620655; CAF06182.1; -
 DR PROSITE; PS50001; SH2; 1.
 DR Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
 KW Transcription regulation.
 FT DOMAIN 580 670 SH2.
 FT MOD RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 FT MOD RES 727 727 Phosphoserine (By similarity).
 SQ SEQUENCE 770 AA; 87974 MW; 9CEB147C73B83274 CRC64;
 Query Match 100.0%; Score 669; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4.6e-54;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IACIGGPPNICLDRLNWTSLAESQLQTRQIKLEELQKVS YKGDPIVQHRPMLER 60
 Db 249 IACIGGPPNICLDRLNWTSLAESQLQTRQIKLEELQKVS YKGDPIVQHRPMLER 308
 Qy 61 IVELFRNLMSAFVVERQPCMPHDPRLVIKTVGQVTTKRLLVKPELNLQIKVKCI 120
 Db 309 IVELFRNLMSAFVVERQPCMPHDPRLVIKTVGQVTTKRLLVKPELNLQIKVKCI 368
 Qy 121 DKDSGDVAA 129
 Db 369 DKDSGDVAA 377
 RESULT 3
 ID STAT3 HUMAN STANDARD; PRT; 770 AA.
 AC P40763; O14916; Q9EW54;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DE Signal transducer and activator of transcription 3 (Acute-phase
 DE response factor).
 DE Name=STAT3; Synonyms=APRF;
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Placenta;
 RA Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
 RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
 RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
 RT related transcription factor involved in the gp130-mediated signaling
 RT pathway."; Cell 77:63-71 (1994).
 RL [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
 RA Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;
 RT "Highly conserved amino-acid sequence between murine STAT3 and a
 RT revised human STAT3 sequence."; Gene 213:119-124 (1998).
 RL [3]
 RP SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
 RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
 RA Rajkumar N., Yi Q., Nickerson D.A.;
 RT "SeattlesNP. NHLBI HL66682 program for genomic applications, UW-
 RT PHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).
 RC TISSUE=Kidney, and Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [5]
 RP SEQUENCE OF 564-704 FROM N.A.
 RC TISSUE=Liver;
 RA Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP PHOSPHORYLATION ON SERINE.
 RX MEDLINE=95215843; PubMed=7701321;
 RA Zhang X., Blienis J., Li H.-C., Schindler C., Chen-Kiang S.;
 RT "Requirement of serine phosphorylation for formation of STAT-promoter
 RT complexes."; Science 267:1990-1994 (1995).
 RL [7]
 RP INTERACTION WITH NCOAL.
 RX PubMed=11773079; DOI=10.1074/jbc.M111486200;
 RA Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
 RT "Functional interaction of STAT3 transcription factor with the
 RT coactivator NCOA/SRC1a."; J. Biol. Chem. 277:8004-8011 (2002).
 CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes.

CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P40763-1; Sequence=Displayed;
 CC Name=Del-701;
 CC IsoId=P40763-2; Sequence=VSP_010474;
 CC TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
 CC muscle, kidney and pancreas
 CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity.
 CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC -----
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 CC -----
 CC EMBL; L29277; AA58374.1; -;
 CC EMBL; AJ012463; CAAL0032.1; -;
 CC EMBL; AY572796; AAS66986.1; -;
 CC EMBL; BC000627; AAH00627.1; -;
 CC EMBL; BC014482; AAH14482.1; -;
 CC EMBL; AF029311; AAB84254.1; -;
 CC PIR; A54444; A54444.
 CC HSP; P42227; LBGI.
 CC TRANSFAC; T01493; -;
 CC Genew; HGNC:11364; STAT3.
 CC H-invDB; HIX0013840; -;
 CC MIM; 102582; -;
 CC GO; GO:0005737; Cytoplasm; TAS.
 CC GO; GO:0005634; Cnucleus; TAS.
 CC GO; GO:0003062; F:hematopoietin/interferon-class (D200-domain...); TAS.
 CC GO; GO:0003700; F:transcription factor activity; TAS.
 CC GO; GO:0006928; P:cell motility; TAS.
 CC GO; GO:0007259; P:JAK-STAT cascade; TAS.
 CC GO; GO:0007399; P:negative regulation of transcription from P...; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR008967; P53_like_DNA_bnd.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001217; STAT.
 CC Pfam; PF00017; SH2; 1.
 CC Pfam; PF01017; STAT_alpha; 1.
 CC Pfam; PF02864; STAT_bind; 1.
 CC Pfam; PF02865; STAT_int; 1.
 CC PROSITE; PS50001; SH2; 1.
 CC Activator; Alternative splicing; DNA-binding; Nuclear protein;
 CC Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
 CC DOMAIN 580 670 SH2.
 CC MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 CC MOD_RES 727 727 Phosphoserine (By similarity).
 CC VARSPPLIC 701 Missing (in isoform Del-701).
 CC /FTId=VSP_010474.
 CC VARIANT 32 32 Q -> K (in dbSNP:1803125).
 CC /FTId=VAR_018683.
 CC VARIANT 143 143 M -> I.
 CC /FTId=VAR_018679.
 CC CONFLICT 288 288 Q -> H (in Ref. 1).
 CC CONFLICT 460 460 P -> S (in Ref. 1).
 CC CONFLICT 548 548 K -> N (in Ref. 1).
 CC CONFLICT 561 561 F -> Y (in Ref. 1).
 CC CONFLICT 667 667 V -> L (in Ref. 1).

FT CONFLICT 730 730 T -> A (in Ref. 1).
 SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
 Query Match 100.0%; Score 669; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4.6e-54;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IACIGPPNICLDRLNENWITSLAESOLQTRQIKKLEELQKKVSYKGDPTVQHRPMLER 60
 |||||
 Db 249 IACIGPPNICLDRLNENWITSLAESOLQTRQIKKLEELQKKVSYKGDPTVQHRPMLER 308
 |||||
 QY 61 IVELPRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKVKCI 120
 |||||
 Db 309 IVELPRLMKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPELNYQLKVKCI 368
 |||||
 QY 121 DKDSGDVAA 129
 |||||
 Db 369 DKDSGDVAA 377
 |||||
 RESULT 4
 STA3 MOUSE
 ID STA3 MOUSE STANDARD; PRT; 770 AA.
 AC P42227;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3 (Acute-phase
 DE response factor).
 GN Name=Stat3; Synonyms=Aprf;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
 RP AND 632-640.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
 RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
 RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
 RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
 RT related transcription factor involved in the gp130-mediated signaling
 RT pathway.";
 RL Cell 77:63-71 (1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC TISSUE=Thymus;
 RX MEDLINE=94188718; PubMed=8140422;
 RA Zhong Z., Wen Z., Darnell J.E. Jr.;
 RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
 RT response to epidermal growth factor and interleukin-6.";
 RL Science 264:95-98 (1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC TISSUE=Brain;
 RX MEDLINE=95014185; PubMed=7523373;
 RA Raz R., Durbin J.E., Levy D.E.;
 RT "Acute phase response factor and additional members of the interferon-
 RT stimulated gene factor 3 family integrate diverse signals from
 RT cytokines, interferons, and growth factors.";
 RL J. Biol. Chem. 269:24391-24395 (1994).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3B).
 RC STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
 RX MEDLINE=96016116; PubMed=7568080;
 RA Schaefer T.S., Sanders L.K., Nathans D.;
 RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
 RT form of Stat3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101 (1995).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC STRAIN=129/SVJ;


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FT STRAND 338 340
FT TURN 341 342
FT STRAND 345 351

Query Match 100.0%; Score 669; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.6e-54;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCI 120
Db 309 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 5
STA3 RAT STANDARD; PRT; 770 AA.
AC P52631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name=Stat3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=liv;
RX MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998;
RA Ripberger J.A., Fritz S., Richter K., Hocke G.M., Lottgepeich F.,
RA Fey G.H.;
RT "Transcription factors Stat3 and Stat5b are present in rat liver
RT nuclei late in an acute phase response and bind interleukin-6 response
RT elements.";
RL J. Biol. Chem. 270:29998-30006(1995).
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes.
CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOA1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation (By similarity).
CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X91810; CAAC2920.1; -
CC DR HSSP; P42227; 1BG1.
CC DR RGD; 3772; Stat3.
CC DR InterPro; IPR008967; P53_like_DNA_bnd.
CC DR InterPro; IPR000980; SH2.
CC DR InterPro; IPR001217; STAT.
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DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS00001; SH2; 1.
KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
KW Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
SQ SEQUENCE 770 AA; 88039 MW; D74AOC76954754ED CRC64;

Query Match 99.6%; Score 666; DB 1; Length 770;
Best Local Similarity 99.2%; Pred. No. 8.7e-54;
Matches 128; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCI 120
Db 309 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCI 368
QY 121 DKDSGDVAA 129
Db 369 DKDSGDVAA 377

RESULT 6
Q6DV79 PRELIMINARY; PRT; 771 AA.
AC Q6DV79;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Signal transducer and activator of transcription 3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G.Y., Leung F.C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF641397; AAT64887.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS00001; SH2; 1.
SQ SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;

Query Match 99.4%; Score 665; DB 2; Length 771;
Best Local Similarity 99.2%; Pred. No. 1.1e-53;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 60
Db 249 IACIGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLER 308
QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCI 120
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Db 309 IVELFRNLKMSAFVVERQPCMPMPHDPRLVFKTGQVQFTTKVRLLVKPELNYQLKIKVCI 368
 QY 121 DKDSGDVAA 129
 Db 369 DKDSGDVAA 377

RESULT 7

Q9PVX8 PRELIMINARY; PRT; 769 AA.
 AC Q9PVX8;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Stat 3.
 GN Name=stat 3;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 CX NCB1_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
 RA Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
 RA Asashima M., Yokota T.;
 RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
 RT embryos independent of BMP-4.";
 RL Dev. Biol. 216:481-490(1999).
 DR EMBL; AB017701; BAA86061.1; -.
 DR HSP; P42227; IBG1.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53 like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF000017; SH2; 1.
 DR Pfam; PF01017; STAT alpha; 1.
 DR Pfam; PF02864; STAT bind; 1.
 DR Pfam; PF02865; STAT int; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS50001; SH2; 1.
 SQ SEQUENCE 769 AA; 87974 MW; 0905C03263303069 CRC64;

Query Match 98.4%; Score 658; DB 2; Length 769;
 Best Local Similarity 98.4%; Pred. No. 4.9e-53;
 Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 IACIGGPPNICLDLENWITSLAESQLQTRQIKKLEELQKYSYKGDPIVQHRPMLER 60
 Db 249 IACIGGPPNICLDLENWITSLAESQLQTRQIKKLEELQKYSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPMPHDPRLVFKTGQVQFTTKVRLLVKPELNYQLKIKVCI 120
 Db 309 IVELFRNLKMSAFVVERQPCMPMPHDPRLVFKTGQVQFTTKVRLLVKPELNYQLKIKVCI 368

QY 121 DKDSGDVAA 129

Db 369 DKDSGDVAA 377

RESULT 8

Q7ZXK3 PRELIMINARY; PRT; 766 AA.
 AC Q7ZXK3;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Stat3-A protein.
 GN Name=stat3-A;

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 CX NCB1_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Kjausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Yettam A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC04717; AAH4717.1; -.
 DR HSP; P42227; IBG1.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53 like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF000017; SH2; 1.
 DR Pfam; PF01017; STAT alpha; 1.
 DR Pfam; PF02864; STAT bind; 1.
 DR Pfam; PF02865; STAT int; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS50001; SH2; 1.
 SQ SEQUENCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;

Query Match 97.2%; Score 650; DB 2; Length 766;
 Best Local Similarity 96.9%; Pred. No. 2.7e-52;
 Matches 125; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IACIGGPPNICLDLENWITSLAESQLQTRQIKKLEELQKYSYKGDPIVQHRPMLER 60
 Db 249 IACIGGPPNICLDLENWITSLAESQLQTRQIKKLEELQKYSYKGDPIVQHRPMLER 308

QY 61 IVELFRNLKMSAFVVERQPCMPMPHDPRLVFKTGQVQFTTKVRLLVKPELNYQLKIKVCI 120
 Db 309 IVELFRNLKMSAFVVERQPCMPMPHDPRLVFKTGQVQFTTKVRLLVKPELNYQLKIKVCI 368

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QY 121 DKDSGDVAA 129
Db 369 DKDSGEGAA 377

RESULT 9
Q7ZTS5 PRELIMINARY; PRT; 414 AA.
ID Q7ZTS5
AC Q7ZTS5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat3 protein.
GN Name=stat3;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny P.J., McKernan K.J., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Young A.C., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
EMBL: BC045276; AAH45276.1; -.
DR HSSP; P42227; 1BG1.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 414 AA; 48253 MW; 0FFD1B509B7526BD CRC64;

Query Match 95.2%; Score 637; DB 2; Length 414;
Best Local Similarity 93.8%; Pred. No. 2.2e-51;
Matches 121; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLENWITSLSAQSLQTRQKIKLEELQKQSYKGDPIVQHRPMLER 60
Db 250 IACIGPPNICLDRLENWITSLSAQSLQTRQKIKLEELQKQSYKGDPIVQHRPMLER 309
QY 61 IVELFRNLKMSAFVVERQPCMHDPRLVIKTVQVTTKRLLVKPELNYQLKIKVCI 120
Db 1 IVELFRNLKMSAFVVERQPCMHDPRLVIKTVQVTTKRLLVKPELNYQLKIKVCI 120
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Db 250 IACIGPPNICLDRLTWTSLAESQLQIRQIRKLEELQOKVSYKGDPIIQRPALEEK 309
QY 61 IVELFRNLKSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 120
Db 310 IVDLFRNLKSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 369
QY 121 DKDSGDVAA 129
Db 370 DKESGDVAA 378

RESULT 11
Q93599 PRELIMINARY; PRT; 806 AA.
AC Q93599
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oates A.C.;
RL Thesis (1998), University of Melbourne, Australia.
DR EMBL; AJ005693; CAA06677.1; -.
DR HSSP; P42227; 1EG1.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; PS3_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;

Query Match 95.28; Score 637; DB 2; Length 806;
Best Local Similarity 93.8%; Pred. No. 4.8e-51;
Matches 121; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 IACIGPPNICLDRLTWTSLAESQLQIRQIRKLEELQOKVSYKGDPIIQRPALEEK 60
Db 250 IACIGPPNICLDRLTWTSLAESQLQIRQIRKLEELQOKVSYKGDPIIQRPALEEK 309
QY 61 IVELFRNLKSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 120
Db 310 IVDLFRNLKSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 369
QY 121 DKDSGDVAA 129
Db 370 DKESGDVAA 378

RESULT 12
Q6DVF3 PRELIMINARY; PRT; 765 AA.
AC Q6DVF3
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Signal transducer and activation of transcription factor 3.

OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641434; AAT46364.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; PS3_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 765 AA; 87566 MW; F5D01408748EC703 CRC64;
Query Match 94.9%; Score 635; DB 2; Length 765;
Best Local Similarity 93.8%; Pred. No. 7e-51;
Matches 121; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 IACIGPPNICLDRLTWTSLAESQLQIRQIRKLEELQOKVSYKGDPIIQRPALEEK 60
Db 250 IACIGPPNICLDRLTWTSLAESQLQIRQIRKLEELQOKVSYKGDPIIQRPALEEK 309
QY 61 IVELFRNLKSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 120
Db 310 IVDLFRNLKSAFVVERQPCMPMPDRPLVKTGQVTTKVRLLVKKPELNYQLKIKVCI 369
QY 121 DKDSGDVAA 129
Db 370 DKESGDVAA 378

RESULT 13
Q6GUE7 PRELIMINARY; PRT; 785 AA.
AC Q6GUE7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Signal transducer and activator of transcription 3 isoform 1.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641434; AAT46364.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; PS3_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
SQ SEQUENCE 785 AA; 87566 MW; F5D01408748EC703 CRC64;


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DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 785 AA; 89643 MW; 81F231BDE27DE338 CRC64;

Query Match          94.9%; Score 635; DB 2; Length 785;
Best Local Similarity 93.8%; Pred. No. 7.2e-51;
Matches 121; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESOLQTRQIKKLEELQKKVSYKGDPIVQHRPMLER 60
   |||||
Db 250 IACIGPPNICLDRLNWTSLAESOLQTRQIKKLEELQKKVSYKGDPIVQHRPMLER 309
   |||||

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
   |||||
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 369
   |||||

QY 121 DKDSGDVAA 129
   |||||
Db 370 DKESGDVAA 378

RESULT 14
Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FFEL8BEFD8BE CRC64;

Query Match          93.3%; Score 624; DB 2; Length 764;
Best Local Similarity 92.2%; Pred. No. 7.5e-50;
Matches 119; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESOLQTRQIKKLEELQKKVSYKGDPIVQHRPMLER 60
   |||||
Db 250 IACIGPPNICLDRLNWTSLAESOLQTRQIKKLEELQKKVSYKGDPIVQHRPMLER 309
   |||||

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
   |||||
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 369
   |||||

QY 121 DKDSGDVAA 129
   |||||
Db 370 DKESGDVAA 378

RESULT 15
O13133 PRELIMINARY; PRT; 767 AA.
AC O13133;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat3.
GN Name=rbStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
SEQUENCE FROM N.A.
RA Johnson M.C., Mourin D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AAB60926.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;

Query Match          89.7%; Score 600; DB 2; Length 767;
Best Local Similarity 89.9%; Pred. No. 1.3e-47;
Matches 116; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 IACIGPPNICLDRLNWTSLAESOLQTRQIKKLEELQKKVSYKGDPIVQHRPMLER 60
   |||||
Db 250 IACIGPPNICLDRLNWTSLAEIQLQIRQIKKLEELQKKVSYKGDPIVQHRPMLER 309
   |||||

QY 61 IVELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 120
   |||||
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPELNYQLKIKVCI 369
   |||||

QY 121 DKDSGDVAA 129
   |||||
Db 370 DKESGDVAA 378

Search completed: May 25, 2005, 17:43:41
Job time : 53.6753 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:14:45 ; Search time 51.0983 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-25
Perfect score: 494
Sequence: 1 KLEELQOKSVYKGDPIVQH.....LNYOLKIKVCIDKDSGDVAA 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

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Database : A_Geneseq_16Dec04 :
1: Geneseqpi1980s : *
2: Geneseqpi1990s : *
3: Geneseqpi2000s : *
4: Geneseqpi2001s : *
5: Geneseqpi2002s : *
6: Geneseqpi2003s : *
7: Geneseqpi2003bs : *
8: Geneseqpi2004s : *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Query		DB	ID	Description
			Match	Length			
1	494	100.0	96	4	AAy72857	AAy72857 Mouse Sta	
2	494	100.0	129	4	AAy72856	AAy72856 Mouse Sta	
3	494	100.0	185	4	AAy72855	AAy72855 Mouse Sta	
4	494	100.0	223	4	AAy72854	AAy72854 Mouse Sta	
5	494	100.0	271	4	AAy72841	AAy72841 Mouse Sta	
6	494	100.0	720	5	AAE222055	AAE222055 Human Sta	
7	494	100.0	769	5	ABBS7164	ABBS7164 Mouse lsc	
8	494	100.0	769	5	AAE222054	AAE222054 Human Sta	
9	494	100.0	769	5	AAE222056	AAE222056 Human pro	
10	494	100.0	770	2	AAr72082	AAr72082 Mouse Sta	
11	494	100.0	770	2	AAE82995	AAE82995 Mouse liv	
12	494	100.0	770	2	AAW03376	AAW03376 Mouse STA	
13	494	100.0	770	2	AAy03768	AAy03768 Human STA	
14	494	100.0	770	3	AAAB12377	AAAB12377 N-termi	
15	494	100.0	770	5	AAE14652	AAE14652 Murine ST	
16	494	100.0	770	5	ABG69497	ABG69497 Human bai	
17	494	100.0	770	6	ABU010476	ABU010476 Mouse STA	
18	494	100.0	770	8	ADN04365	ADN04365 Antipsori	
19	494	100.0	770	8	ADP54789	ADP54789 Human PRO	
20	494	100.0	793	3	AAE58442	AAE58442 Lung canc	
21	491	99.4	770	7	ADD44738	ADD44738 Rat Prote	
22	489	99.0	770	2	AAE82993	AAE82993 Human pla	
23	489	99.0	770	4	AAAB19964	AAAB19964 Human sig	
24	489	99.0	770	5	AAE15174	AAE15174 Human Sta	
25	489	99.0	770	7	ADD44740	ADD44740 Human PRO	

ALIGNMENTS

RESULT 1

AAAY72857

ID AAY72857 standard; protein; 96 AA.

AA72857:

31-MAY-2001 (first entry)

DE Mouse Stat3 protein fragment

Mouse: Stat3 protein: transcription factor; c-Jun: gene

KW cellular transformation, dysproliferative disease, cancer, psoriasis;
KW therapy.

XX
: 1999

OS Mus musculus.

FH **Key**

```

ET
region
Stat3-c-Jun
/note= "Stat3-c-Jun

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FT 342-358

XX
PN WO200116605-A2.

08-MAR-2001.

30-AUG-2000:

XX
PR 31-AUG-1999: 99UIS-00387418XX
PA (INBO) INTIV BOCKFEELLER

XX DT Zhang Y. Housath C. W.

[illegible]

XX

PT transcription factor c-Jun and a Stat3 protein.

XX 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 104

XX

CC amino acids of Stat3 protein. The invention relates to methods for
CC identifying interacting regions of transcription factors and methods for
CC identifying agents which modulates the interaction between a Stat-1 and
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A

CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX Sequence 96 AA;

Query Match 100.0%; Score 494; DB 4; Length 96;
 Best Local Similarity 100.0%; Pred. No. 3.6e-55;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVIKT 60
 DB 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVIKT 60

QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
 DB 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96

RESULT 2
 AAY72856
 ID AAY72856 standard; protein; 129 AA.
 XX
 AC AAY72856;
 DT
 DT 31-MAY-2001 (first entry)
 XX
 DE Mouse Stat3 protein fragment #14 (249-377 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FH Region 94..110
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 XX WO200116605-A2.
 XX
 XX 08-MAR-2001.
 XX
 XX 30-AUG-2000; 2000WO-US023822.
 XX
 XX 31-AUG-1999; 99US-00387418.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 XX
 XX Identifying an agent for use in modulating the interaction between
 XX transcription factor c-Jun and a Stat3 protein.
 XX
 XX Claim 65; Page 80-81; 86pp; English.
 XX
 XX The present sequence is mouse Stat3 protein fragment containing 249-377
 XX amino acids of Stat3 protein. The invention relates to methods for
 XX identifying interacting regions of transcription factors and methods for
 XX identifying agents which modulates the interaction between a
 XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 XX Stat-3, useful for modulating gene transcription e.g., cellular
 XX dysproliferative diseases and also for treating cancer and psoriasis. A
 XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 XX binding domain, linker domain, SH2 domain and transactivation domain
 XX Sequence 129 AA;

Query Match 100.0%; Score 494; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 5.2e-55;

QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVIKT 60
 DB 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVIKT 60

QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
 DB 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVIKT 60
 DB 34 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVIKT 93

QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
 DB 94 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 129

RESULT 3
 AAY72855
 ID AAY72855 standard; protein; 185 AA.
 XX
 AC AAY72855;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Mouse Stat3 protein fragment #13 (193-377 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FH Region 150..166
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 XX WO200116605-A2.
 XX
 XX 08-MAR-2001.
 XX
 XX 30-AUG-2000; 2000WO-US023822.
 XX
 XX 31-AUG-1999; 99US-00387418.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 XX
 XX Identifying an agent for use in modulating the interaction between
 XX transcription factor c-Jun and a Stat3 protein.
 XX
 XX Claim 65; Page 80; 86pp; English.
 XX
 XX The present sequence is mouse Stat3 protein fragment containing 193-377
 XX amino acids of Stat3 protein. The invention relates to methods for
 XX identifying interacting regions of transcription factors and methods for
 XX identifying agents which modulates the interaction between a
 XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 XX Stat-3, useful for modulating gene transcription e.g., cellular
 XX dysproliferative diseases and also for treating cancer and psoriasis. A
 XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 XX binding domain, linker domain, SH2 domain and transactivation domain
 XX Sequence 185 AA;

Query Match 100.0%; Score 494; DB 4; Length 185;
 Best Local Similarity 100.0%; Pred. No. 8.4e-55;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVIKT 60
 DB 90 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMPHDPRLVIKT 149

QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96

Db 150 GVQFTTKVRLLVKFPPELVQKIKVCIDKSGDVA 185
|||||
RESULT 4
AA72854
ID AAY72854 standard; protein; 223 AA.
XX AAY72854;
AC AAY72854;
XX 31-MAY-2001 (first entry)
XX Mouse Stat3 protein fragment #12 (155-377 amino acids).
DE Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX Mus musculus.
XX Key Location/Qualifiers
FT Region 188..204
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX WO200116605-A2.
XX 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023822.
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX Claim 65; Page 79; 86pp; English.
XX The present sequence is mouse Stat3 protein fragment containing 155-377
CC amino acids of Stat3 protein. The invention relates to methods for
CC identifying interacting regions of transcription factors and methods for
CC identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
SQ Sequence 223 AA;
Query Match 100.0%; Score 494; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLEELQOKVSYKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 128 KKLEELQOKVSYKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 187
QY 61 GVQFTTKVRLLVKFPPELVQKIKVCIDKSGDVA 96
Db 188 GVQFTTKVRLLVKFPPELVQKIKVCIDKSGDVA 223
RESULT 5
AA72841
ID AAY72841 standard; protein; 271 AA.
XX AAY72841;
AC AAY72841;
XX 31-MAY-2001 (first entry)
XX Mouse Stat3 protein fragment #2 (107-377 amino acids).
DE Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX Mus musculus.
XX Key Location/Qualifiers
FT Region 24..48
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
XX 236..252
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX WO200116605-A2.
XX 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023822.
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein.
XX Claim 65; Page 67-68; 86pp; English.
XX The present sequence is mouse Stat3 protein fragment containing 107-377
CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
CC to c-Jun protein in the cell extract. The invention relates to methods
CC for identifying interacting regions of transcription factors and methods
CC for identifying agents which modulates the interaction between a
CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
CC Stat-3, useful for modulating gene transcription e.g., cellular
CC transformation. These identifying agents are used in the treatment of
CC dysproliferative diseases and also for treating cancer and psoriasis. A
CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
CC binding domain, linker domain, SH2 domain and transactivation domain
SQ Sequence 271 AA;
Query Match 100.0%; Score 494; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.4e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLEELQOKVSYKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 176 KKLEELQOKVSYKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 235
QY 61 GVQFTTKVRLLVKFPPELVQKIKVCIDKSGDVA 96
Db 236 GVQFTTKVRLLVKFPPELVQKIKVCIDKSGDVA 271
RESULT 6
AAE22055
ID AAE22055 standard; protein; 720 AA.
XX AAE22055;
AC AAE22055;
XX

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKEELQKQVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPHDPRLVIKT 60
 DB 282 KKEELQKQVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPHDPRLVIKT 341
 QY 61 GVOFTTKVRLLVKFPPELVOLKIKVCIDKDSGDVAA 96
 DB 342 GVOFTTKVRLLVKFPPELVOLKIKVCIDKDSGDVAA 377

RESULT 8
 AAE22054
 ID AAE22054 standard; protein; 769 AA.
 XX
 AC AAE22054;
 XX
 DT 25-JUL-2002 (first entry)
 XX
 DE Human Stat3 protein.
 XX
 KW Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.
 XX
 OS Homo sapiens.
 XX
 XX WO200220032-A1.
 PN
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028254.
 XX
 PR 08-SEP-2000; 2000US-0231212P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 PI Yu H, Pardoll D, Jove R, Dalton W;
 XX
 XX WPI; 2002-362218/39.
 DR N-PSDB; AAD35065.
 XX
 PT Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.
 XX
 PS Disclosure; Page 83-85; 94pp; English.
 XX
 CC The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,

CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human Stat3
 CC protein
 XX
 SQ Sequence 769 AA;

Query Match 100.0%; Score 494; DB 5; Length 769;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKEELQKQVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPHDPRLVIKT 60
 DB 282 KKEELQKQVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPHDPRLVIKT 341
 QY 61 GVOFTTKVRLLVKFPPELVOLKIKVCIDKDSGDVAA 96
 DB 342 GVOFTTKVRLLVKFPPELVOLKIKVCIDKDSGDVAA 377

RESULT 9
 AAE22056
 ID AAE22056 standard; protein; 769 AA.
 XX
 AC AAE22056;
 XX
 DT 25-JUL-2002 (first entry)
 XX
 DE Human protein related to angiogenesis regulation.
 XX
 KW Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.
 XX
 OS Homo sapiens.
 XX
 XX WO200220032-A1.
 PN
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028254.
 XX
 PR 08-SEP-2000; 2000US-0231212P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 PI Yu H, Pardoll D, Jove R, Dalton W;
 XX
 XX WPI; 2002-362218/39.
 DR
 PT Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT compound that modulates the activity of a signal transducer and activator

PT of transcription 3.
 PS Disclosure; Page 83-85; 94pp; English.
 XX
 CC The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC protein related to angiogenesis regulation
 XX
 SQ Sequence 769 AA;

Query Match 100.0%; Score 494; DB 5; Length 769;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLLELOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKT 60
 DB 282 KKLLELOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKT 341
 QY 61 GVQFTTKVRLLVKFPPELVQKIKVCIDKDSGDVAA 96
 DB 342 GVQFTTKVRLLVKFPPELVQKIKVCIDKDSGDVAA 377

RESULT 10
 AAR72082
 ID AAR72082 standard; protein; 770 AA.
 XX
 AC AAR72082;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX
 DE Mouse Stat3 (19sf6).
 XX
 KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
 KW receptor recognition factor; transcription factor; cellular debilitation;
 KW derangement; dysfunction; interferon-gamma.
 XX
 OS Mus sp.
 XX
 PN W09508629-A1.
 XX
 PD 30-MAR-1995.
 XX
 PF 26-SEP-1994; 94WO-US010849.
 XX
 PR 24-SEP-1993; 93US-00126588.
 PR 24-SEP-1993; 93US-00126595.

PR 11-MAR-1994; 94US-00212184.
 PR 11-MAR-1994; 94US-00212185.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 XX
 DR WPI; 1995-139598/18.
 DR N-PSDB; AAQ89340.
 XX
 PT Receptor recognition factor implicated in transcriptional stimulation of
 PT genes - useful in drug screening assays and/or for treating cellular
 PT debilitations, derangements and/or dysfunctions, etc.
 XX
 PS Claim 1; Page 107-110; 160pp; English.
 XX
 CC A fragment encoding the human Stat3 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
 CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC -40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed
 CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 770 AA;
 Query Match 100.0%; Score 494; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLLELOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKT 60
 DB 282 KKLLELOQKVSXKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVIKT 341
 QY 61 GVQFTTKVRLLVKFPPELVQKIKVCIDKDSGDVAA 96
 DB 342 GVQFTTKVRLLVKFPPELVQKIKVCIDKDSGDVAA 377

RESULT 11
 AAR82995
 ID AAR82995 standard; protein; 770 AA.
 XX
 AC AAR82995;
 XX
 DT 25-MAR-1996 (first entry)
 XX
 DE Mouse liver acute phase response factor.
 XX
 KW Mouse; acute phase response factor; transcription factor; interleukin-6;
 KW signal transduction; liver; antibody; antitumor; antitumor; antitumor;
 KW antiinflammatory; antitumor; antitumor; antitumor; antitumor; antitumor;
 XX
 OS Mus musculus.
 XX
 PN EP676469-A2.
 XX
 PD 11-OCT-1995.
 XX
 PF 29-MAR-1995; 95BP-00104670.
 XX
 PR 04-APR-1994; 94JP-00065825.
 XX
 PA (KISH/) KISHIMOTO T.
 XX
 PI Akira S, Kishimoto T;
 XX
 DR WPI; 1995-346089/45.
 DR N-PSDB; AAT05619.
 XX
 PT New acute phase response factor - for developing inhibitory agents for

PT treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
 PT diseases.

PS Claim 10; Page 20-22; 31pp; English.

XX The sequence represents a mouse acute phase response factor (APRF), a
 CC transcription factor related to signal transmission of interleukin-6 (IL-
 CC 6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
 CC library using a polymerase chain reaction product (amplified using
 CC primers derived from an IL-6-treated mouse liver peptide) as a probe.
 CC APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
 CC ribozymes, may be used to treat diseases induced by IL-6, e.g.
 CC inflammatory disease, leukemia, cancer, osteoclastia, pulmonary
 CC hypertension, etc

XX Sequence 770 AA;

SQ Query Match 100.0%; Score 494; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPMPHDPRLVIKT 60
 Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPMPHDPRLVIKT 341

OY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
 Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 12

AAW03176

ID AAW03176 standard; protein; 770 AA.

XX AC AAW03176;

DT 24-OCT-1996 (first entry)

XX Mouse STAT4.

KW STAT; STAT4; signal transducer and activator of transcription;
 KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
 KW autoimmune disease; antagonist; therapy.

XX Mus sp.

EH Key Location/Qualifiers

FT Domain 398..508

FT /label= DNA_binding_domain

FT /note= "Claim 3, page 110"

XX WO9620954-A2.

XX 11-JUL-1996.

XX 28-DEC-1995; 95WO-US017025.

XX 06-JAN-1995; 95US-00369796.

XX (UYRQ) UNIV ROCKEFELLER.

XX Darnell JE, Wen Z, Horvath CM, Zhong Z;

XX WPI; 1996-333941/33.

XX N-PSDB; AAT31280.

XX New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,
 PT preventing or treating cellular dysfunction, e.g. oncogenesis,
 PT inflammation, parasitic disease or autoimmunity.

XX Disclosure; Page 87-90; 138pp; English.

XX Mouse signal transducer and activator of transcription (STAT) protein

CC STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from
 CC ligand-activated receptor kinase complexes followed by nuclear
 CC translocation and DNA binding to activate transcription. Recombinant
 CC STAT4 can be obtd. using cDNA clone 19af6 (AAT31278) obtd. from
 CC splenic/thymic cells. STAT4 includes a DNA-binding domain (see also
 CC AAW03167) capable of both receptor recognition and message delivery via
 CC DNA binding in a receptor-ligand specific manner. STAT proteins and their
 CC DNA binding domains (see also AAW03165-75) are useful for screening
 CC antagonists used to inhibit STAT-mediated signal transduction and
 CC activation of transcription

XX Sequence 770 AA;

SQ Query Match 100.0%; Score 494; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPMPHDPRLVIKT 60
 Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFENLMKSAFVVERQPCMPMPHDPRLVIKT 341

OY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
 Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 13

AAW03768

ID AAW03768 standard; protein; 770 AA.

XX AC AAW03768;

XX 11-JUN-1999 (first entry)

XX Human STAT3 allelic variant.

KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;
 KW intracellular transcription factor; interleukin-6; medicament; variant;
 KW pharmaceutical; autoimmune disease; inflammatory; human.

XX Homo sapiens.

XX EP905234-A2.

XX 31-MAR-1999.

XX 18-FEB-1998; 98EP-00102774.

XX 16-SEP-1997; 97EP-00116061.

XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Serlupi-Crescenzi O, Della Pietra L;

XX WPI; 1999-192864/17.

XX N-PSDB; AAX29281.

XX New human Signal Transducer and Activator of Transcription 3 (STAT3)
 PT allelic variant useful for treatment of autoimmune and inflammatory
 PT disease.

XX Claim 2; Page 9-13; 32pp; English.

XX The present sequence represents a predominant allelic variant of human
 CC Signal Transducer and Activator of Transcription 3 (STAT3) protein, an
 CC intracellular transcription factor which mediates IL-6 signals. The
 CC encoding sequence differs from the original published human STAT3 gene
 CC sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3
 CC DNA molecule can be used for the recombinant expression of the variant.
 CC STAT3 protein is useful as a medicament or pharmaceutical composition for
 CC treatment of autoimmune or inflammatory diseases

XX Sequence 770 AA;

Query Match 100.0%; Score 494; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKT 60
 DB 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKT 341
 QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
 DB 342 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 14
 AAB12377
 ID AAB12377 standard; peptide; 770 AA.
 XX
 AC AAB12377;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE N-terminal domain of murine STAT-3 protein.
 XX
 KW STAT; signal transducer and activator of transcription; crystal;
 KW drug design; murine.
 XX
 OS Mus sp.

Key	Location/Qualifiers
FT Region	4..9
FT Region	/label= Alpha helix 1
FT Region	12..21
FT Region	/label= Alpha helix 2
FT Region	19..21
FT Region	/label= 3(10) helix of alpha helix 2
FT Region	28..33
FT Region	/label= Alpha helix 3
FT Region	35..40
FT Region	/label= Alpha helix 4
FT Region	43..47
FT Region	/label= Alpha helix 5
FT Region	50..73
FT Region	/label= Alpha helix 6
FT Region	77..96
FT Region	/label= Alpha helix 7
FT Region	99..119
FT Region	/label= Alpha helix 8

US6087478-A.
 11-JUL-2000.
 23-JAN-1998; 98US-00012710.
 23-JAN-1998; 98US-00012710.
 (UYRQ) UNIV ROCKEFELLER.
 Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
 WPI; 2000-505108/45.

New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development.
 Disclosure; Fig 1; 42pp; English.
 The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts X-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater

than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structural structure determined for the crystal

Sequence 770 AA;

Query Match 100.0%; Score 494; DB 3; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.3e-54;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKT 60
 DB 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCMPMPDRPLVIKT 341
 QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
 DB 342 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 15
 AAE14652
 ID AAE14652 standard; protein; 770 AA.
 XX
 AC AAE14652;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE Murine STAT3 protein.
 XX
 KW Signal transducer and activator of transcription; STAT3;
 KW drug development; drug discovery; crystal; inflammation; allergy; asthma;
 KW leukaemia; anaemia; neutropenia; thrombocytopaenia; cancer; obesity;
 KW viral disease; growth retardation; murine.

Key	Location/Qualifiers
FT Domain	1..130
FT	/note= "Conserved N-terminal domain of the STAT family"

US6312887-B1.
 06-NOV-2001.
 24-APR-2000; 2000US-00556273.
 23-JAN-1998; 98US-00012710.
 (UYRQ) UNIV ROCKEFELLER.
 Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
 WPI; 2002-033337/04.

Identifying compounds that bind to signal transducer and activator of transcription proteins, useful for the production of new drugs.
 Example; Col 47-50; 44pp; English.

The invention relates to methods for detecting compounds that bind to signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural properties of the protein crystal. The methods include: identifying a compound that binds to the N-terminal domain of a STAT protein, identifying a compound that enhances or diminishes the binding of the dimeric STAT proteins to each other and/or their nucleic acid binding site; or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new

CC drugs. An antagonist of STAT N-terminal dimeric interactions that
CC inhibits the binding of the STAT dimers to adjacent weak binding sites on
CC a promoter of a gene, could be useful as drugs in the treatment of
CC diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other
CC hand, an agonist of N-terminal dimeric interactions between STAT dimers,
CC can be used as drugs in the treatment of diseases e.g. anaemia,
CC neutropenia, thrombocytopaenia, cancer, obesity, viral diseases and
CC growth retardation. The present sequence is murine STAT3 protein
XX

SQ Sequence 770 AA;

Query Match 100.0%; Score 494; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.3e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQKQVSYKGDPIVQHRPMLLEERIVELFRNLKMSAFVVERQPCMPHDPDRPLVIKT 60
|||
Db 282 KLEELQKQVSYKGDPIVQHRPMLLEERIVELFRNLKMSAFVVERQPCMPHDPDRPLVIKT 341
|||

QY 61 GVQFTTKVRLLVKPPPELNYQLKIKVCIDKDSGDVAA 96
|||
Db 342 GVQFTTKVRLLVKPPPELNYQLKIKVCIDKDSGDVAA 377
|||

Search completed: May 25, 2005, 17:36:36
Job time : 51.265 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 12.0119 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-25
Perfect score: 494
Sequence: 1 KXLEELQKVSXKGDPIVQH.....LNQLKIKVICDKSGDVAA 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B-COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCUTS-COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score		Query Match	Length	DB	ID	Description
	%						
1	494	100.0	96	3	US-09-387-418A-25	Sequence 25, Appl	
2	494	100.0	129	3	US-09-387-418A-24	Sequence 24, Appl	
3	494	100.0	185	3	US-09-387-418A-23	Sequence 23, Appl	
4	494	100.0	223	3	US-09-387-418A-22	Sequence 22, Appl	
5	494	100.0	271	3	US-09-387-418A-9	Sequence 9, Appl	
6	494	100.0	770	1	US-08-369-796-12	Sequence 12, Appl	
7	494	100.0	770	1	US-08-416-581B-9	Sequence 9, Appl	
8	494	100.0	770	2	US-08-852-091-12	Sequence 12, Appl	
9	494	100.0	770	2	US-08-820-754-12	Sequence 12, Appl	
10	494	100.0	770	3	US-08-956-652-12	Sequence 12, Appl	
11	494	100.0	770	3	US-08-956-869-12	Sequence 12, Appl	
12	494	100.0	770	3	US-09-012-710-8	Sequence 8, Appl	
13	494	100.0	770	3	US-08-948-547-12	Sequence 12, Appl	
14	494	100.0	770	3	US-09-364-970-3	Sequence 3, Appl	
15	494	100.0	770	3	US-09-364-970-5	Sequence 5, Appl	
16	494	100.0	770	3	US-09-556-273-8	Sequence 8, Appl	
17	494	100.0	770	3	US-08-956-653A-12	Sequence 12, Appl	
18	494	100.0	770	3	US-09-526-542-2	Sequence 2, Appl	
19	494	100.0	770	4	US-08-212-185-12	Sequence 12, Appl	
20	494	100.0	770	4	US-10-117-087-2	Sequence 2, Appl	
21	494	100.0	770	5	PCT-US95-17025-12	Sequence 12, Appl	
22	489	99.0	770	1	US-08-416-581B-1	Sequence 1, Appl	
23	489	99.0	770	1	US-08-416-581B-5	Sequence 5, Appl	
24	489	99.0	770	3	US-09-087-465-6	Sequence 6, Appl	
25	489	99.0	770	4	US-09-372-800A-6	Sequence 6, Appl	
26	489	99.0	771	1	US-08-276-099A-14	Sequence 14, Appl	
27	489	99.0	771	1	US-08-781-890-14	Sequence 14, Appl	

28	396	80.2	229	3	US-09-387-418A-18	Sequence 18, Appl
29	396	80.2	229	3	US-09-387-418A-28	Sequence 28, Appl
30	396	80.2	229	3	US-09-387-418A-30	Sequence 30, Appl
31	396	80.2	229	3	US-09-387-418A-31	Sequence 31, Appl
32	396	80.2	252	3	US-09-387-418A-14	Sequence 14, Appl
33	379	76.7	229	3	US-09-387-418A-29	Sequence 29, Appl
34	318	64.4	213	3	US-09-387-418A-19	Sequence 19, Appl
35	318	64.4	236	3	US-09-387-418A-15	Sequence 15, Appl
36	310	62.8	268	3	US-09-387-418A-12	Sequence 12, Appl
37	310	62.8	582	4	US-09-430-806A-3	Sequence 3, Appl
38	310	62.8	712	1	US-08-369-796-6	Sequence 6, Appl
39	310	62.8	712	2	US-08-852-091-6	Sequence 6, Appl
40	310	62.8	712	2	US-08-820-754-6	Sequence 6, Appl
41	310	62.8	712	3	US-08-956-652-6	Sequence 6, Appl
42	310	62.8	712	3	US-08-956-869-6	Sequence 6, Appl
43	310	62.8	712	3	US-08-948-547-6	Sequence 6, Appl
44	310	62.8	712	3	US-08-956-653A-6	Sequence 6, Appl
45	310	62.8	712	4	US-08-212-185-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-387-418A-25
; Sequence 25, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissea H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 25
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-25

Query Match		100.0%;	Score 494;	DB 3;	Length 96;
Best Local Similarity		100.0%;	Pred. No. 4.3e-54;		
Matches	96;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1	KXLEELQKVSXKGDPIVQHRPMLERIIVELFRLMKSAFVVERQPCMPMHPDRPLVIKT 60			
Db	1	KXLEELQKVSXKGDPIVQHRPMLERIIVELFRLMKSAFVVERQPCMPMHPDRPLVIKT 60			
Qy	61	GVQFTTKVRLLVKFPPELNYQLKIKVICDKSGDVAA 96			
Db	61	GVQFTTKVRLLVKFPPELNYQLKIKVICDKSGDVAA 96			

RESULT 2
US-09-387-418A-24
; Sequence 24, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissea H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-24

Query Match      100.0%; Score 494; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 6.3e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60
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Db 34 KLEELQOKVSYKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 93
    |||

QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
    |||
Db 94 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 129
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RESULT 3
US-09-387-418A-23
; Sequence 23, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-23

Query Match      100.0%; Score 494; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 1e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60
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Db 90 KLEELQOKVSYKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 149
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QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
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Db 150 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 185
    |||

RESULT 4
US-09-387-418A-22
; Sequence 22, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 223
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-22

Query Match      100.0%; Score 494; DB 3; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60
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Db 128 KLEELQOKVSYKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 187
    |||

QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
    |||
Db 188 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 223
    |||

RESULT 5
US-09-387-418A-9
; Sequence 9, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-9

Query Match      100.0%; Score 494; DB 3; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.7e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQOKVSYKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60
    |||
Db 176 KLEELQOKVSYKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 235
    |||

QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
    |||
Db 236 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 271
    |||

RESULT 6
US-08-369-796-12
; Sequence 12, Application US/08369796
; Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-369-796-12

Query Match 100.0%; Score 494; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPHDPRLVIKT 60
DB 282 KKLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPHDPRLVIKT 341
QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
DB 342 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 7
US-08-416-581B-9
Sequence 9, Application US/08416581B
Patent No. 5719042
GENERAL INFORMATION:
APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR APRF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-65825/1994
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-37891
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-416-581B-9
Query Match 100.0%; Score 494; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPHDPRLVIKT 60
DB 282 KKLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPHDPRLVIKT 341
QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
DB 342 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 8
US-08-852-091-12
Sequence 12, Application US/08852091
Patent No. 5883228
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-091-12

Query Match 100.0%; Score 494; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPHDPRLVIKT 60
DB 282 KKLEELQOKVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPHDPRLVIKT 341

QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
 |||||
 Db 342 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 9
 US-08-820-754-12
 ; Sequence 12, Application US/08820754
 ; Patent No. 5976835
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan
 ; APPLICANT: Wen, Zhong
 ; APPLICANT: Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/820,754
 ; FILING DATE: 19-MAR-1997
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,185
 ; FILING DATE: 11-MAR-1994
 ; APPLICATION NUMBER: US 07/980,498
 ; FILING DATE: 23-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/854,296
 ; FILING DATE: 19-MAR-1992
 ; APPLICATION NUMBER: WO US93/02569
 ; FILING DATE: 19-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/126,588
 ; FILING DATE: 24-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-820-754-12

Query Match 100.0%; Score 494; DB 2; Length 770;
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 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLEELQOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 60
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 Db 282 KLEELQOKSVYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 341

QY 61 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
 |||||
 Db 342 GVOFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 10
 US-08-956-652-12
 ; Sequence 12, Application US/08956652
 ; Patent No. 6013475
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan
 ; APPLICANT: Wen, Zhong
 ; APPLICANT: Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/956,652
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,185
 ; FILING DATE: 11-MAR-1994
 ; APPLICATION NUMBER: US 07/980,498
 ; FILING DATE: 23-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/854,296
 ; FILING DATE: 19-MAR-1992
 ; APPLICATION NUMBER: WO US93/02569
 ; FILING DATE: 19-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/126,588
 ; FILING DATE: 24-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-956-652-12

Query Match 100.0%; Score 494; DB 3; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.4e-53;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 342 GVQFTTKVRLVLPPELVQLKIKVCIDKSGDVAA 377

RESULT 11
US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-956-869-12

Query Match 100.0%; Score 494; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 282 KKLEELQKVSYGDPVQHRPMLERIVELFNLKMSAFVVERQPCMPHDPRLVIKT 341
QY 61 GVQFTTKVRLVLPPELVQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLVLPPELVQLKIKVCIDKSGDVAA 377

RESULT 12
US-09-012-710-8
; Sequence 8, Application US/09012710
; Patent No. 6087478
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-012-710-8
Query Match 100.0%; Score 494; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLEELQKVSYGDPVQHRPMLERIVELFNLKMSAFVVERQPCMPHDPRLVIKT 60
Db 282 KKLEELQKVSYGDPVQHRPMLERIVELFNLKMSAFVVERQPCMPHDPRLVIKT 341
QY 61 GVQFTTKVRLVLPPELVQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLVLPPELVQLKIKVCIDKSGDVAA 377

RESULT 13
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klauber & Jackson
;; STREET: 411 Hackensack Avenue
;; CITY: Hackensack
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07601
;; COMPUTER READABLE FORM: disk
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/948,547
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/212,185
;; FILING DATE: 11-MAR-1994
;; APPLICATION NUMBER: US 07/980,498
;; FILING DATE: 23-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/854,296
;; FILING DATE: 19-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO US93/02569
;; FILING DATE: 19-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/126,588
;; FILING DATE: 24-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 770 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-948-547-12

Query Match 100.0%; Score 494; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 282 KKLEELQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 341

QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 14
US-09-364-970-3
; Sequence 3, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPLIOPERATIVE CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT APPLICATION NUMBER: US/09/364,970
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-364-970-5

Query Match 100.0%; Score 494; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 282 KKLEELQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 341

QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

Search completed: May 25, 2005, 17:47:39
Job time : 13.0119 secs

;; SEQ ID NO 3
;; LENGTH: 770
;; TYPE: PRT
;; ORGANISM: Mus musculus
;; US-09-364-970-3

Query Match 100.0%; Score 494; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 15
US-09-364-970-5
; Sequence 5, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPLIOPERATIVE CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT APPLICATION NUMBER: US/09/364,970
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-364-970-5

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Best Local Similarity 100.0%; Pred. No. 6.4e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 282 KKLEELQKVSXKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 341

QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

Search completed: May 25, 2005, 17:47:39
Job time : 13.0119 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:36:58 ; Search time 42.0417 Seconds
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Perfect score: 494
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	494	100.0	129	13	US-10-090-185-24
3	494	100.0	185	13	US-10-090-185-23
4	494	100.0	223	13	US-10-090-185-22
5	494	100.0	271	13	US-10-090-185-21
6	494	100.0	720	15	US-10-380-020-4
7	494	100.0	769	15	US-10-380-020-2
8	494	100.0	769	15	US-10-380-020-5
9	494	100.0	770	11	US-10-045-793-12
10	494	100.0	770	14	US-10-045-792-8
11	494	100.0	770	14	US-10-038-010-56
12	494	100.0	770	14	US-10-117-087-2
13	494	100.0	770	17	US-10-639-617-12

14	494	100.0	793	9	US-09-925-302-780	Sequence 780, App
15	494	100.0	793	10	US-09-925-302-780	Sequence 780, App
16	491	99.4	770	15	US-10-116-275-329	Sequence 329, App
17	489	99.0	770	15	US-10-116-275-349	Sequence 349, App
18	396	80.2	229	13	US-10-090-185-18	Sequence 18, App
19	396	80.2	229	13	US-10-090-185-28	Sequence 28, App
20	396	80.2	229	13	US-10-090-185-30	Sequence 30, App
21	396	80.2	229	13	US-10-090-185-31	Sequence 31, App
22	396	80.2	252	13	US-10-090-185-14	Sequence 14, App
23	379	76.7	229	13	US-10-090-185-29	Sequence 29, App
24	318	64.4	213	13	US-10-090-185-19	Sequence 19, App
25	318	64.4	236	13	US-10-090-185-15	Sequence 15, App
26	311	63.0	749	9	US-09-833-205-4	Sequence 4, Appli
27	310	62.8	268	13	US-10-090-185-12	Sequence 12, Appl
28	310	62.8	582	14	US-10-245-120-3	Sequence 3, Appli
29	310	62.8	712	11	US-09-876-773-6	Sequence 6, Appli
30	310	62.8	712	14	US-10-245-120-2	Sequence 2, Appli
31	310	62.8	712	17	US-10-639-617-6	Sequence 6, Appli
32	310	62.8	712	17	US-10-936-390-5	Sequence 5, Appli
33	310	62.8	750	9	US-09-833-205-2	Sequence 2, Appli
34	310	62.8	750	11	US-09-876-773-4	Sequence 1, Appli
35	310	62.8	750	14	US-10-245-120-1	Sequence 1, Appli
36	310	62.8	750	14	US-10-308-279-44	Sequence 44, Appl
37	310	62.8	750	16	US-10-755-889-352	Sequence 352, App
38	310	62.8	750	16	US-10-755-889-823	Sequence 823, App
39	310	62.8	750	17	US-10-492-043-19	Sequence 19, Appl
40	310	62.8	750	17	US-10-639-617-4	Sequence 4, Appli
41	310	62.8	786	9	US-09-925-297-550	Sequence 550, App
42	291	58.9	423	14	US-10-177-293-437	Sequence 437, App
43	291	58.9	748	14	US-10-177-293-439	Sequence 439, App
44	231	58.9	748	16	US-10-755-889-70	Sequence 70, Appl
45	291	58.9	748	16	US-10-755-889-362	Sequence 362, App

ALIGNMENTS

RESULT 1

US-10-090-185-25
; Sequence 25, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-25

Query Match 100.0%; Score 494; DB 13; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.9e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLEELQKVSXKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPHDPRLVIKT 60
Db 1 KLEELQKVSXKGDPIVQHRPMLERIIVELFNLKMSAFVVERQPCMPHDPRLVIKT 60
Qy 61 GVOFTTKVLLVKFPFLNYQLKIKVICDKSGDVAA 96
Db 61 GVOFTTKVLLVKFPFLNYQLKIKVICDKSGDVAA 96

RESULT 2

US-10-090-185-24
; Sequence 24, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-24

Query Match 100.0%; Score 494; DB 13; Length 129;

Best Local Similarity 100.0%; Pred. No. 4.2e-53; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 0;

Qy 1 KKEELQKQSVYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60

Db 34 KKEELQKQSVYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 93

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIVCIDKDSGDVAA 96

Db 94 GVQFTTKVRLLVKFPPELNYQLKIVCIDKDSGDVAA 129

RESULT 3

US-10-090-185-23
; Sequence 23, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-23

Query Match 100.0%; Score 494; DB 13; Length 185;

Best Local Similarity 100.0%; Pred. No. 6.7e-53; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 0;

Qy 1 KKEELQKQSVYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60

Db 90 KKEELQKQSVYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 149

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIVCIDKDSGDVAA 96

Db 150 GVQFTTKVRLLVKFPPELNYQLKIVCIDKDSGDVAA 185

RESULT 4

US-10-090-185-22
; Sequence 22, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-22

Query Match 100.0%; Score 494; DB 13; Length 223;

Best Local Similarity 100.0%; Pred. No. 8.5e-53; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 0;

Qy 1 KKEELQKQSVYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60

Db 128 KKEELQKQSVYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 187

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIVCIDKDSGDVAA 96

Db 188 GVQFTTKVRLLVKFPPELNYQLKIVCIDKDSGDVAA 223

RESULT 5

US-10-090-185-9
; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-9

Query Match 100.0%; Score 494; DB 13; Length 271;

Best Local Similarity 100.0%; Pred. No. 1.1e-52; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 0;

Qy 1 KKEELQKQSVYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60

Db 176 KKEELQKQSVYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 235

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIVCIDKDSGDVAA 96

	Query Match	100.0%;	Score 494;	DB 15;	Length 769;
	Best Local Similarity	100.0%;	Pred. No. 4.2e-52;	Mismatches 0;	Gaps 0;
	Matches 96;	Conservative 0;			
Oy	1	KKLEELQKVSYKGDP	I VQHRPMLERIEIVELFNLMKSAFVVERQCMPMHDPRLVIKT	60	
Ddb	282	KKLEELQKVSYKGDP	I VQHRPMLERIEIVELFNLMKSAFVVERQCMPMHDPRLVIKT	341	
Oy	61	GVQFTTKVRLLVKFPPELNTQLKIKVCIDKDSGDVA	A 96		
Ddb	342	GVQFTTKVRLLVKFPPELNTQLKIKVCIDKDSGDVA	A 377		

RESULT 9
US-09-876-773-12
; Sequence 12, Application US/09876773
; Publication NO. US20040058318A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,773
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US/07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US/07/854,296

FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12
Query Match 100.0%; Score 494; DB 11; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.2e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLEELQKQVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 282 KLEELQKQVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 341
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377
RESULT 10
US-10-045-792-8
Sequence 8, Application US/10045792
Publication No. US20030003563A1
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
Moarefi, Ismail
Darnell, Jr., James E.
Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/045,792
FILING DATE: 19-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8
Query Match 100.0%; Score 494; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.2e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLEELQKQVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 282 KLEELQKQVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 341
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377
RESULT 11
US-10-038-010-56
Sequence 56, Application US/10038010
Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/259,377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 56
LENGTH: 770
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: STAT3 : Transcription factor
LOCATION: (1)..(770)
OTHER INFORMATION:
US-10-038-010-56
Query Match 100.0%; Score 494; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.2e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLEELQKQVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 282 KLEELQKQVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 341
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377
RESULT 12
US-10-117-087-2
Sequence 2, Application US/10117087
Publication No. US20030166854A1
GENERAL INFORMATION:
APPLICANT: SERLUPI-CRESCENZI, Ottaviano
APPLICANT: DELLA PIETRA, Linda
TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
FILE REFERENCE: SERLUPI=2
CURRENT APPLICATION NUMBER: US/10/117,087

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; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/526,542
; PRIOR FILING DATE: 2000-03-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Human
US-10-117-087-2

Query Match 100.0%; Score 494; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.2e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLKMSAFVVERQPCMPMHPDRPLVIKT 341

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 13
US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/639,617
; FILING DATE: 12-Aug-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

Query Match 100.0%; Score 494; DB 17; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.2e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLKMSAFVVERQPCMPMHPDRPLVIKT 341

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 377

RESULT 14
US-09-925-302-780
; Sequence 780, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match 100.0%; Score 494; DB 9; Length 793;
Best Local Similarity 100.0%; Pred. No. 4.3e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 305 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLNLKMSAFVVERQPCMPMHPDRPLVIKT 364

Qy 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
Db 365 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 400

RESULT 15
US-09-925-302-780
; Sequence 780, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
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; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

Query Match      100.0%; Score 494; DB 10; Length 793;
Best Local Similarity 100.0%; Pred. No. 4.3e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLLELOQKVSYGKGDPIVQHRPMLLEERIVELFRNLKMSAFVVERQPCMPHDPRLVIKT 60
Db 305 ||||| 305 KKLLELOQKVSYGKGDPIVQHRPMLLEERIVELFRNLKMSAFVVERQPCMPHDPRLVIKT 60

Qy 61 GVQFTTKVRLLVKFPPELVNQLKIKVCIDKDSGDVAA 96
Db 365 GVQFTTKVRLLVKFPPELVNQLKIKVCIDKDSGDVAA 400
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Search completed: May 25, 2005, 18:21:52
Job time : 43.375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:24:07 ; Search time 9.0566 Seconds

(without alignments)
1019.898 Million cell updates/sec

Title: US-10-090-185-25

Perfect score: 494

Sequence: 1 KLEELQKVS YKGDPIVQH.....LNQLKIKVICDKSGDVAA 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	494	100.0	770	2 I49508	ISGF3 p91-related
2	489	99.0	770	2 A54444	DNA-binding protein
3	310	62.8	739	2 A46159	interferon-depende
4	283	57.3	748	2 A56047	gamma-interferon a
5	204	41.3	851	2 A46160	interferon alpha-i
6	90.5	18.3	848	2 A54740	interleukin-4-indu
7	86.5	17.5	786	2 I49274	mammary gland fact
8	86.5	17.5	793	2 S54772	mammary gland fact
9	86.5	17.5	794	2 G02317	transcription acti
10	86.5	17.5	794	2 S55527	mammary gland fact
11	83.5	16.9	837	2 I57357	DNA-Binding Protei
12	72	14.6	393	2 S32458	4-hydroxyphenylpyr
13	72	14.6	393	2 S32821	4-hydroxyphenylpyr
14	71	14.4	498	2 T06667	argininosuccinate
15	68	13.8	363	2 S48483	MRS1 protein - yea
16	68	13.8	590	2 A48461	ovarian abundant m
17	68	13.8	1152	2 E71667	2-acetylglucosamin
18	67	13.6	376	2 S32820	allotransferrin F - ra
19	67	13.6	402	2 T29703	hypothetical prote
20	67	13.6	415	2 JCT167	C kinase 1 interac
21	67	13.6	508	2 AF1479	fatty-acid-CoA lig
22	66	13.4	376	2 A60236	F protein - mouse
23	66	13.4	393	2 T25063	hypothetical prote
24	66	13.4	508	2 AC1119	fatty-acid-CoA lig
25	65.5	13.3	748	2 T47250	complex I intermed
26	65.5	13.3	926	2 T39082	hypothetical prote
27	64	13.0	334	1 DEBYMM	malate dehydrogena
28	64	13.0	364	2 T30084	hypothetical prote
29	64	13.0	460	2 H89907	hypothetical prote

30 63.5 12.9 395 2 T43892 translation elonga
31 63 12.8 416 2 A56486 perinuclear bindin
32 63 12.8 695 2 T39954 probable gpase ac
33 62.5 12.7 339 2 T41126 meiotic recombina
34 62.5 12.7 378 1 S42088 mevalonate kinase
35 62.5 12.7 781 2 T39373 dynamin-related pr
36 62.5 12.7 804 2 B84389 ribonucleoside red
37 62 12.6 307 1 PNB5L beta-lactamase (EC
38 62 12.6 328 2 A99345 conserved hypothet
39 62 12.6 369 2 T21556 hypothetical prote
40 62 12.6 580 2 C71182 probable ABC trans
41 62 12.6 1493 2 A38218 GAP-associated pro
42 61.5 12.4 191 2 B70042 hypothetical prote
43 61.5 12.4 256 2 T48076 60S RIBOSOMAL PROT
44 61.5 12.4 451 2 S73433 pre-B cell enhanci
45 61.5 12.4 451 2 B81056 proteinase, probab

ALIGNMENTS

RESULT 1

I49508

ISGF3 p91-related transcription factor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49508; I49009

R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su

Cell 77, 63-71, 1994

A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr

A;Reference number: A54444, MUID:94208062; PMID:7512451

A;Accession: I49508

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-770 <RES>

A;Cross-references: UNIPROT:P42227; GB:L29278; NID:G476715; PIDN:AAA37254.1; PID:G47671

R;Raz, R.; Durbin, J.E.; Levy, D.E.

J. Biol. Chem. 269, 24391-24395, 1994

A;Title: Acute phase response factor and additional members of the interferon-stimulate

A;Reference number: I49009; MUID:95014185; PMID:7523373

A;Accession: I49009

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-393, 'M', 395-700, 702-770 <RE2>

A;Cross-references: EMBL:U08378; NID:G473889; PIDN:AAA56668.1; PID:G473890

C;Genetics:

A;Gene: APRF

C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 100.0%; Score 494; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.6e-46;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQKVS YKGDPIVQH R PML EERIVEL FPNLMKSAFVVERQCPMPHPDRLVIKT 60
Db 282 KLEELQKVS YKGDPIVQH R PML EERIVEL FPNLMKSAFVVERQCPMPHPDRLVIKT 341

QY 61 GVQFTTKVRLLVKFPPELNLQKIKVICDKSGDVAA 96

Db 342 GVQFTTKVRLLVKFPPELNLQKIKVICDKSGDVAA 377

RESULT 2

A54444

DNA-binding protein APRF - human

C;Species: Homo sapiens (man)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C;Accession: A54444

R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su

Cell 77, 63-71, 1994

A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr

A;Reference number: A54444; MUID:94208062; PMID:7512451

A;Accession: A54444

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:G475788; PID:G475789
C;Genetics:
A;Gene: GDB:STAT3; APRF
A;Cross-references: GDB:358950
A;Map position: 17q21-17q21
A;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor

Query Match 99.0%; Score 489; DB 2; Length 770;
Best Local Similarity 99.0%; Pred. No. 1.6e-45;
Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60
DB 282 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 341
QY 61 GVOFTTKVRLLVKPELNYQLKIKVCIDKSGDVAA 96
DB 342 GVOFTTKVRLLVKPELNYQLKIKVCIDKSGDVAA 377

RESULT 3
A46159
interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Improt, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91- and 84-kDa ISGF-3
A;Reference number: A46159; MUID:92366557; PMID:1502203
A;Accession: A46159
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
A;Cross-references: UNIPROT:P42224
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 62.8%; Score 310; DB 2; Length 739;
Best Local Similarity 64.4%; Pred. No. 6.6e-26;
Matches 58; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60
DB 267 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 326
QY 61 GVOFTTKVRLLVKPELNYQLKIKVCIDK 90
DB 327 GVOFTTKVRLLVKPELNYQLKIKVCIDK 356

RESULT 4
A56047
gamma-interferon activation site-binding protein Stat4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, M.; Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in ea
A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-748 <YAM>
A;Cross-references: UNIPROT:P42228; GB:U09351; NID:G509502; PID:AAA19692.1; PID:G509503
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein

Query Match 57.3%; Score 283; DB 2; Length 748;
Best Local Similarity 58.9%; Pred. No. 6.1e-23;
Matches 53; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 1 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60
DB 277 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 336
QY 61 GVOFTTKVRLLVKPELNYQLKIKVCIDK 90
DB 337 LIOFTVKRLRLVQLKPELNYQLKIKVCIDK 366

RESULT 5
A46160
interferon alpha-induced transcription activator ISGF-3, 113K chain - human
N;Alternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908: S53873
R;Fu, X.Y.; Schindler, C.; Improt, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator
A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-851 <FUL>
A;Cross-references: UNIPROT:P52630
A;Note: sequence extracted from NCBI backbone (NCBIP:110820)
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell, J.E.
submitted to the EMBL data library, December 1994
A;Reference number: S71908
A;Accession: S71908
A;Molecule type: DNA
A;Residues: 1-851 <YAN>
A;Cross-references: EMBL:U18671; NID:G1293919; PIDN:AAA98760.1; PID:G1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in
A;Reference number: S53873; MUID:95192056; PMID:7885841
A;Accession: S53873
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-196;392-591;684-730 <YAN>
A;Cross-references: EMBL:U18671
C;Genetics:
A;Gene: stat2
A;Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; 4
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: signal transduction; transcription regulation

Query Match 41.3%; Score 204; DB 2; Length 851;
Best Local Similarity 44.4%; Pred. No. 3.3e-14;
Matches 40; Conservative 19; Mismatches 31; Indels 0; Gaps 0;

QY 1 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 60
DB 277 KKLLEELQKVSXKGDPTVQHRPMLERIVELFRLNLMKSAFVVERQPCMPMHPDRPLVIKT 336
QY 61 GVOFTTKVRLLVKPELNYQLKIKVCIDK 90
DB 337 GSKFTVTRTLVRLQGNESLTVESIDRN 366

RESULT 6
A54740
interleukin-4-induced transcription factor stat - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54740
R;Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.

[illegible]

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:15:30 ; Search time 39.9444 Seconds
(without alignments)
1230.701 Million cell updates/sec

Title: US-10-090-185-25
Perfect score: 494
Sequence: 1 KLEELQKQVSYKGDPIVQH.....LNYQLKIKVICDKSGDVAA 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	494	100.0	163	Q9N145	Q9N145 macaca mula
2	494	100.0	770	1 STA3 BOVIN	P61635 bos taurus
3	494	100.0	770	1 STA3 HUMAN	P40763 homo sapien
4	494	100.0	770	1 STA3 MOUSE	P42227 mus musculus
5	491	99.4	770	1 STA3 RAT	P52631 rattus norv
6	490	99.2	771	2 Q6DV79	Q6dv79 gallus gall
7	489	99.0	769	2 Q9PVX8	Q9pvx8 xenopus lae
8	487	98.6	161	2 Q704W5	Q704w5 bos taurus
9	475	96.2	766	2 Q7ZXX3	Q7zxx3 xenopus lae
10	474	96.0	414	2 Q7ZTS5	Q7zt55 brachydanio
11	474	96.0	786	2 Q6NV46	Q6nv46 brachydanio
12	474	96.0	806	2 Q93599	Q93599 brachydanio
13	472	95.5	765	2 Q6DVU7	Q6dvf3 oryzias lat
14	472	95.5	785	2 Q6GUE7	Q6gue7 oryzias lat
15	461	93.3	764	2 Q90V16	Q90v16 tetraodon f
16	453	91.7	767	2 Q13133	Q13133 oncorhynch
17	315	63.8	751	2 Q8JGNO	Q8jgn0 xenopus lae
18	311	63.0	712	2 Q6P6Q7	Q6p6q7 rattus norv
19	311	63.0	749	2 Q8C497	Q8c497 mus musculus
20	311	63.0	749	2 Q9QXK0	Q9qxk0 rattus norv
21	310	62.8	712	2 Q9K9K4	Q9kk94 mus musculus
22	310	62.8	749	2 Q8C3V4	Q8c3v4 mus musculus
23	310	62.8	749	2 Q8D323	Q8d323 mus musculus
24	310	62.8	750	1 STA1 HUMAN	P42224 homo sapien
25	310	62.8	750	2 Q68D00	Q68d00 homo sapien
26	310	62.8	755	2 Q8C8M3	Q8cm3 mus musculus
27	309	62.6	758	2 Q90Y17	Q90y17 tetraodon f
28	304	61.5	757	2 Q764M5	Q764m5 sus scrofa
29	294	59.5	1153	2 Q8JF85	Q8jfs5 brachydanio
30	292	59.1	754	2 Q13131	Q13131 oncorhynch
31	292	59.1	754	2 Q13132	Q13132 oncorhynch

RESULT 1

Q9N145 ID Q9N145 PRELIMINARY; PRT; 163 AA.
AC Q9N145; 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Signal transducer and activator of transcription (Fragment).
GN Name=STAT3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J.
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF227560; AAF73401.1; -
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR NON_TER 1
FT NON_TER 163
FT NON_TER 163
SQ SEQUENCE 163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;

Query Match 100.0%; Score 494; DB 2; Length 163;

Best Local Similarity 100.0%; Pred. No. 1.3e-46;

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLEELQKQVSYKGDPIVQHRLPMLERIVLFELFNLKMSAFVVERQPCWMPHDPRLVIKT 60

Db 52 KLEELQKQVSYKGDPIVQHRLPMLERIVLFELFNLKMSAFVVERQPCWMPHDPRLVIKT 111

QY 61 GVQFTTKVRLLVKFPPELVOLKIKVICDKSGDVAA 96

Db 112 GVQFTTKVRLLVKFPPELVOLKIKVICDKSGDVAA 147

RESULT 2

STA3_BOVIN ID STA3_BOVIN STANDARD; PRT; 770 AA.
AC P61635;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.

GN Name=STAT3;
OS Bos taurus (Bovine).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Mammary gland;
RC Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
RA "The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus
RT during ruminant evolution.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes (By similarity).
CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation (By similarity).
CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC
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CC or send an email to license@sb-sib.ch).
CC
CC EMBL: AJ620655; CAP06182.1; -
DR PROSITE; PSS0001; SH2; 1.
KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
RN Transcription regulation.
FT DOMAIN 580 670
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
SQ SEQUENCE 770 AA; 87974 MW; 9CEB147C73EB3274 CRC64;

Query Match 100.0%; Score 494; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 7.7e-46;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLEELQKYSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 60
Db 282 KLEELQKYSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 341

Qy 61 GVQFTTKVRLVLPPELNYQLKIKVCIDKDSGDVAA 96
Db 342 GVQFTTKVRLVLPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 3
STA3 HUMAN
ID STA3 HUMAN STANDARD; PRT; 770 AA.
AC P40763; O14916; Q9BW54;
DT 01-FEB-1995 (Rel. 31, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
DE response factor).
GN Name=STAT3; Synonyms=APRF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Placenta;
RC Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RX Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,

RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
RT related transcription factor involved in the gp130-mediated signaling
RT pathway.";
RL Cell 77:63-71(1994).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
RA Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;
RT "Highly conserved amino-acid sequence between murine STAT3 and a
RT revised human STAT3 sequence.";
RL Gene 213:119-124(1998).
[3]
RN SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
RP Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattlesNPs. NHDBI HU66882 program for genomic applications, UW-
RT FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).
RP TISSUE=Kidney, and Pancreas;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN SEQUENCE OF 564-704 FROM N.A.
RP TISSUE=Liver;
RC Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;
RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
[6]
RN PHOSPHORYLATION ON SERINE.
RP MEDLINE=95215843; PubMed=7701321;
RX Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
RT "Requirement of serine phosphorylation for formation of STAT-promoter
RT complexes.";
RL Science 267:1990-1994 (1995).
[7]
RN INTERACTION WITH NCOAL.
RP PubMed=11773079; DOI=10.1074/jbc.M11486200;
RX Girard S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
RT "Functional interaction of STAT3 transcription factor with the
RT coactivator NcoA/SRC1a.";
RL J. Biol. Chem. 277:8004-8011(2002).
CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes.
CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC

CC IsoId=P40763-1; Sequence=Displayed;
 CC Name=Del-701;
 CC ISOId=P40763-2; Sequence=VSP_010474;
 CC TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
 CC muscle, kidney and pancreas.
 CC -1- PPM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity.
 CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -----
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 CC EMBL; L29277; AAA58374.1; -;
 CC EMBL; AJ012463; CAA10032.1; -;
 CC EMBL; AY572796; AAS66986.1; -;
 CC EMBL; BC000627; AAH00627.1; -;
 CC EMBL; BC014482; AAH14482.1; -;
 CC EMBL; AF029311; AAB84254.1; -;
 CC PIR; A54444; A54444.
 CC HSSP; P42227; IBL1.
 CC TRANSFAC; T01493; -;
 CC Genew; HGNC.11364; STAT3.
 CC H-InvDB; HIX0013840; -;
 CC MIM; 102582; -;
 CC GO; GO:0005737; C:cytoplasm; TAS.
 CC GO; GO:0005634; C:nucleus; TAS.
 CC GO; GO:0005052; F:hematopoietin/interferon-class (D200-domain. .; TAS.
 CC GO; GO:0003700; F:transcription factor activity; TAS.
 CC GO; GO:0006928; P:cell motility; TAS.
 CC GO; GO:0007259; P:JAK-STAT cascade; TAS.
 CC GO; GO:0001222; P:negative regulation of transcription from P. .; TAS.
 CC GO; GO:0007399; P:neurogenesis; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR008967; P53_like_DNA_bnd.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001217; STAT.
 CC Pfam; PF00017; SH2; 1.
 CC Pfam; PF01017; STAT_alpha; 1.
 CC Pfam; PF02864; STAT_bind; 1.
 CC Pfam; PF02865; STAT_int; 1.
 CC PROSITE; PS00001; SH2; 1.
 CC KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
 CC Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
 CC DOMAIN 580 670
 CC MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 CC MOD_RES 727 727 Phosphoserine (By similarity).
 CC VARSPPLIC 701 701 Missing (in isoform Del-701).
 CC FTID=VSP_010474.
 CC Q -> K (in dbSNP:1803125).
 CC /FTID=VAR_018683.
 CC M -> I.
 CC /FTID=VAR_018679.
 CC Q -> H (in Ref. 1).
 CC P -> S (in Ref. 1).
 CC K -> N (in Ref. 1).
 CC F -> Y (in Ref. 1).
 CC V -> L (in Ref. 1).
 CC T -> A (in Ref. 1).
 CC SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
 Query Match 100.0%; Score 494; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 7.7e-46;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLEELQOKVSYKGDPIVQHRPMLERIVELFRLMKSAFVVERQPCMPHDPRLVIKT 60

Db 282 KKLEELQOKVSYKGDPIVQHRPMLERIVELFRLMKSAFVVERQPCMPHDPRLVIKT 341
 QY 61 GVQFTTKVRLLVKFPPELVQKIKVCIDKSDGVAA 96
 Db 342 GVQFTTKVRLLVKFPPELVQKIKVCIDKSDGVAA 377
 RESULT 4
 STAT3 MOUSE
 ID STAT3_MOUSE STANDARD; PRT; 770 AA.
 AC P42227;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3 (Acute-phase
 DE response factor).
 GN Name:Stat3; Synonyms=Aprf;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
 RP AND 632-640.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
 RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsueaka T.,
 RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
 RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
 RT related transcription factor involved in the gp130-mediated signaling
 RT pathway.";
 RL Cell 77:63-71(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC TISSUE=Thymus;
 RX MEDLINE=94188718; PubMed=8140422;
 RA Zhong Z., Wen Z., Darnell J.E. Jr.;
 RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
 RT response to epidermal growth factor and interleukin-6.";
 RL Science 264:95-98(1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC TISSUE=Brain;
 RX MEDLINE=95014185; PubMed=7523373;
 RA Raz R., Durbin J.E., Levy D.E.;
 RT "Acute phase response factor and additional members of the interferon-
 RT stimulated gene factor 3 family integrate diverse signals from
 RT cytokines, interferons, and growth factors.";
 RL J. Biol. Chem. 269:24391-24395(1994).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3B).
 RC STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
 RX MEDLINE=96016116; PubMed=7568080;
 RA Schaefer T.S., Sanders L.K., Nathans D.;
 RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
 RT form of Stat3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC STRAIN=129/SVJ;
 RX PubMed=11161808; DOI=10.1006/geno.2000.6433;
 RA Miyoshi K., Cui Y., Riedlinger G., Lehoczy J., Zon L., Oka T.,
 RA Dewar K., Hennighausen L.;
 RT "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
 RT zebrafish to mouse.";
 RL Genomics 71:150-155(2001).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC STRAIN=C57BL/6J, and NOD/LtJ;
 RA Davoodi-Semiromi A., She J.-X.;
 RT "A mutant Stat3b with weaker DNA binding defines a key defective
 RT pathway in non-obese diabetic (NOD) mice.";

Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

[7]
SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=FVB/N; TISSUE=Hammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Butterfield Y.S.N., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Smailus D.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS
RX MEDLINE=95344205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
RA Wen Z., Zhong Z., Darnell J.E. Jr.;
RT "Maximal activation of transcription by Stat1 and Stat3 requires both
RT tyrosine and serine phosphorylation.";
RL Cell 82:241-250(1995).
[9]
X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
RX MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
RA Becker S., Groner B., Mueller C.W.;
RT "Three-dimensional structure of the Stat3beta homodimer bound to
RT DNA.";
RL Nature 394:145-151(1998).
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes. STAT3B interacts with the N-terminal
CC part of JUN to activate such promoters in a cooperative way.
CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Stat3A.
CC IsoId=P42227-1; Sequence=Displayed;
CC Name=Stat3B;
CC IsoId=P42227-2; Sequence=VSP_006287;
CC Name=Del-701;
CC IsoId=P42227-3; Sequence=VSP_010475;
CC -!- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
CC kidney. STAT3B is also detected in the liver, although in a much
CC less abundant manner.
CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.

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CC entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).

CC DR EMBL; L29278; AAA37254.1; -;
DR EMBL; U06922; AAA19452.1; -;
DR EMBL; U08378; AAA56668.1; -;
DR EMBL; U30709; AAC5262.1; -;
DR EMBL; AF246978; AAL59017.1; -;
DR EMBL; AY299489; AAQ75418.1; -;
DR EMBL; AY299490; AAQ75419.1; -;
DR EMBL; BC003806; AAH03806.1; -;
DR PIR; I49508; I49508;
DR PDB; 1BGL; X-ray; A=1-722.
DR TRANSFAC; T01574; -;
DR MGD; MGI:103038; Stat3.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0003677; F:DNA binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016563; F:transcriptional activator activity; IDA.
DR GO; GO:0007259; P:JAK-STAT cascade; IDA.
DR GO; GO:0006357; P:regulation of transcription from Pol II pro. .; IDA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PSS0001; SH2; 1.
KW 3D-structure; Activator; Acute phase; Alternative splicing;
KW Direct protein sequencing; DNA-binding; Nuclear protein;
KW Phosphorylation; SH2 domain; Transcription regulation.
FT DOMAIN 580 670
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine.
FT VARSPLOC 716 770 TTCSNTIDLPMSRTLDLSLMQFGNGEAPSPAGQPESLT
FT FMDLTSECATSPM -> FIDAVWK (in isoform
FT Stat3B).
FT /FTId=VSP_006287.
FT Missing (in isoform Del-701).
FT /FTId=VSP_010475.
FT S->A: Decreased transcriptional
FT activation.
FT E -> K (in Ref. 2).
FT S -> T (in Ref. 2 and 4).
FT M -> I (in Ref. 1).

Query Match	100.0%;	Score 494;	DB 1;	Length 770;
Best Local Similarity	100.0%;	Pred. No. 7.7e-46;		
Matches	96;	Conservative	0;	Mismatches 0; Gaps 0;

Oy 1 KCLLELOQKYSYKGDPTVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 60
|||
DB 282 KCLLELOQKYSYKGDPTVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 341
|||

```

Qy 61 GVOFTTKVRLVLPPELNYQLKIKVCIDKDSGDVAA 96
Db 342 GVOFTTKVRLVLPPELNYQLKIKVCIDKDSGDVAA 377

RESULT 5
STA3 RAT
ID _STA3 RAT STANDARD; PRT; 770 AA.
AC PS2631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name=Stat3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96102059; PubMed=8530402; DOI=10.1074/jbc.270.50.29998;
RA Ripberger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,
RA Fey G.H.;
RT "Transcription factors Stat3 and Stat5b are present in rat liver
RT nuclei late in an acute phase response and bind interleukin-6 response
RT elements."
RL J. Biol. Chem. 270:29998-30006(1995).
CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes.
CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation (By similarity).
CC -1- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity (By similarity).
CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X91810; CAA62920.1; -.
DR HSSP; P42227; 1BG1.
DR RGD; 3772; Stat3.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
DR Activator; DNA-binding, Nuclear protein; Phosphorylation; SH2 domain;
KW Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
SQ SEQUENCE 770 AA; 88039 MW; D74A0C76954754ED CRC64;

Query Match 99.4%; Score 491; DB 1; Length 770;
Best Local Similarity 99.0%; Pred. No. 1.7e-45;
Matches 95; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLMKSAFVVERQPCMPHDPRLVFKT 60
Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVDLFRLMKSAFVVERQPCMPHDPRLVFKT 341

RESULT 7
STA3 RAT
ID _STA3 RAT PRELIMINARY; PRT; 769 AA.
AC Q9PVX8;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DE Signal transducer and activator of transcription 3.
GN Name=stat 3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;

Query Match 99.2%; Score 490; DB 2; Length 771;
Best Local Similarity 99.0%; Pred. No. 2.1e-45;
Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLMKSAFVVERQPCMPHDPRLVFKT 60
Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLMKSAFVVERQPCMPHDPRLVFKT 341

RESULT 8
STA3 RAT
ID _STA3 RAT PRELIMINARY; PRT; 771 AA.
AC Q6DV79;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE Signal transducer and activator of transcription 3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G.Y., Leung F.C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AY641397; AAT64887.1; -.
DR GO; GO:0005634; Cnucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
DR SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;

Query Match 99.2%; Score 490; DB 2; Length 771;
Best Local Similarity 99.0%; Pred. No. 2.1e-45;
Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLMKSAFVVERQPCMPHDPRLVFKT 60
Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRLMKSAFVVERQPCMPHDPRLVFKT 341

RESULT 9
STA3 RAT
ID _STA3 RAT PRELIMINARY; PRT; 769 AA.
AC Q9PVX8;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DE Signal transducer and activator of transcription 3.
GN Name=stat 3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;

Query Match 99.4%; Score 491; DB 1; Length 770;
Best Local Similarity 99.0%; Pred. No. 1.7e-45;
Matches 95; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RA Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
 RA Aaashima M., Yokota T.;
 RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
 RT embryos independent of BMP-4.";
 RL Dev. Biol. 216:481-490(1999).
 DR EMBL; AB017701; BAA86061.1; -.
 DR HSSP; P42227; 1BG1.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53 like_DNA_bnd.
 DR InterPro; IPR000980; SH2
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS0001; SH2; 1.
 SQ SEQUENCE 769 AA; 87974 MW; 0905C03263303069 CRC64;
 Query Match 99.0%; Score 489; DB 2; Length 769;
 Best Local Similarity 99.0%; Pred. No. 2.8e-45;
 Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KKLLEELQKQVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPHDPRLVIKT 60
 DB 282 KKLLEELQKQVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPHDPRLVIKT 341
 QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
 DB 342 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 377
 RESULT 8
 Q704W5 PRELIMINARY; PRT; 161 AA.
 ID Q704W5
 AC Q704W5
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Signal transducer and activator of transcription 3 (Fragment).
 GN Name=stat3;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Mollenaar A., Wheeler T.T., McCracken J.Y., Seyfert H.M.;
 RT "The STAT3-encoding gene resides within the 40 kbp gap between the
 RT STAT5A- and STAT5B-encoding genes in cattle.";
 RL Anim. Genet. 31:333-334(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ620661; CAF06188.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR008967; P53 like_DNA_bnd.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF01017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 FT NON_TER

FT NON_TER 161
 SQ SEQUENCE 161 AA; 18342 MW; 5DCEE8F2C3A48191 CRC64;
 Query Match 98.6%; Score 487; DB 2; Length 161;
 Best Local Similarity 99.0%; Pred. No. 7.7e-46;
 Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KKLLEELQKQVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPHDPRLVIKT 60
 DB 16 KKLLEELQKQVSYKGDPIVQHRPMLERIVELFRLNLMKSAFVVERQPCMPHDPRLVIKT 75
 QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 96
 DB 76 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGDVAA 111
 RESULT 9
 Q7ZXX3 PRELIMINARY; PRT; 766 AA.
 ID Q7ZXX3
 AC Q7ZXX3
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Stat3-A protein.
 GN Name=stat3-A;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC044717; AAH44717.1; -.
 DR HSSP; P42227; 1BG1.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P3_like_DNA_bnd.
 DR InterPro; IPR009080; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS0001; SH2; 1.
 SQ SEQUENCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;

Query Match 96.2%; Score 475; DB 2; Length 766;
 Best Local Similarity 95.8%; Pred. No. 9.7e-44;
 Matches 92; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 60
 :|||||
 Db 282 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 341
 :|||||

Qy 61 GVQFTTKVRLVKFPPELNYQLKIKVCIDKDSGDVAA 96
 :|||||
 Db 342 GVQFTTKVRLVKFPPELNYQLKIKVCIDKDSGDVAA 377
 :|||||

RESULT 10
 Q7ZTS5 PRELIMINARY; PRT; 414 AA.
 AC Q7ZTS5;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Stat3 protein.
 OS Name=stat3;
 GN Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC045276; AAH45276.1; -.
 DR HSSP; P42227; IBGL.
 DR ZFIN; ZDB-GENE-980526-68; stat3.
 DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P3_like_DNA_bnd.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 SQ SEQUENCE 414 AA; 48253 MW; 0FFD1B509B7526BD CRC64;

Query Match 96.0%; Score 474; DB 2; Length 414;
 Best Local Similarity 93.8%; Pred. No. 6.2e-44;
 Matches 90; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 60
 :|||||
 Db 283 KLEELQOKVSYKGDPIVQHRPMLERIVELFRNLKMSAFVVERQPCWMPHDPRLVIKT 342
 :|||||

Qy 61 GVQFTTKVRLVKFPPELNYQLKIKVCIDKDSGDVAA 96
 :|||||
 Db 343 GVQFTTKVRLVKFPPELNYQLKIKVCIDKDSGDVAA 378
 :|||||

RESULT 11
 Q6NV46 PRELIMINARY; PRT; 786 AA.
 AC Q6NV46;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Stat3 protein.
 OS Name=stat3;
 GN Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC068320; AAH68320.1; -.
 DR ZFIN; ZDB-GENE-980526-68; stat3.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.

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DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR008967; P53_like_DNA_bnd.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001217; STAT.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF01017; STAT_alpha; 1.
DR Pfam: PF02864; STAT_bind; 1.
DR Pfam: PF02865; STAT_int; 1.
DR PROSITE: PS0001; SH2; 1.
SQ SEQUENCE 786 AA; 90039 MW; FC7371D0B08E5447E CRC64;
Query Match 96.0%; Score 474; DB 2; Length 786;
Best Local Similarity 93.8%; Pred. No. 1.3e-43;
Matches 90; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 KLEELQKQVSYKGDPIVQHRPMLERIVLFRNLKMSAFVVERQPCMPHDPRLVIKT 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 283 KLEELQKQVSYKGDPIVQHRPMLERIVLFRNLKMSAFVVERQPCMPHDPRLVIKT 342
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 343 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 378
RESULT 12
O93599 PRELIMINARY; PRT; 806 AA.
AC O93599;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RA Oates A.C.;
RL Thesis (1998), University of Melbourne, Australia.
DR HSP; P42227; IBI.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO: 0005634; C:nucleus; IEA.
DR GO: 0003700; F:signal transducer activity; IEA.
DR GO: 0003700; F:transcription factor activity; IEA.
DR GO: 0007242; P:intracellular signaling cascade; IEA.
DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR008967; P53_like_DNA_bnd.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001217; STAT.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF01017; STAT_alpha; 1.
DR Pfam: PF02864; STAT_bind; 1.
DR Pfam: PF02865; STAT_int; 1.
DR SMART; SMO0252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3942 CRC64;
Query Match 96.0%; Score 474; DB 2; Length 806;
Best Local Similarity 93.8%; Pred. No. 1.3e-43;
Matches 90; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 KLEELQKQVSYKGDPIVQHRPMLERIVLFRNLKMSAFVVERQPCMPHDPRLVIKT 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 283 KLEELQKQVSYKGDPIVQHRPMLERIVLFRNLKMSAFVVERQPCMPHDPRLVIKT 342
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 343 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 378
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RESULT 13
O6DVF3 PRELIMINARY; PRT; 765 AA.
AC O6DVF3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Signal transducer and activation of transcription factor 3.
DE Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Beloniformes; Adrianchthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
SEQUENCE FROM N.A.
RA Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY639947; AAT64912.1; -.
DR GO: 0005634; C:nucleus; IEA.
DR GO: 0004871; F:signal transducer activity; IEA.
DR GO: 0003700; F:transcription factor activity; IEA.
DR GO: 0007242; P:intracellular signaling cascade; IEA.
DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR008967; P53_like_DNA_bnd.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001217; STAT.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF01017; STAT_alpha; 1.
DR Pfam: PF02864; STAT_bind; 1.
DR Pfam: PF02865; STAT_int; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 765 AA; 87566 MW; F5D01408748EC703 CRC64;
Query Match 95.5%; Score 472; DB 2; Length 765;
Best Local Similarity 93.8%; Pred. No. 2.1e-43;
Matches 90; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 KLEELQKQVSYKGDPIVQHRPMLERIVLFRNLKMSAFVVERQPCMPHDPRLVIKT 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 283 KLEELQKQVSYKGDPIVQHRPMLERIVLFRNLKMSAFVVERQPCMPHDPRLVIKT 342
QY 61 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 96
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 343 GVQFTTKVRLLVKFPPELNYQLKIKVCIDKSGDVAA 378
RESULT 14
O6GUE7 PRELIMINARY; PRT; 785 AA.
AC O6GUE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Signal transducer and activator of transcription 3 isoform 1.
DE Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Beloniformes; Adrianchthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
SEQUENCE FROM N.A.
RA Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641434; AAT46364.1; -.
DR GO: 0005634; C:nucleus; IEA.
DR GO: 0004871; F:signal transducer activity; IEA.
DR GO: 0003700; F:transcription factor activity; IEA.
DR GO: 0007242; P:intracellular signaling cascade; IEA.
DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR008967; P53_like_DNA_bnd.
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DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 785 AA; 89643 MW; 81F231BDE27DE938 CRC64;

Query Match          95.5%; Score 472; DB 2; Length 785;
Best Local Similarity 93.8%; Pred. No. 2.2e-43;
Matches 90; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLEELQKQVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 283 KLEELQKQVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 342

Qy 61 GVQFTTKVRLLVKFPPELNYQLKVCIDKDSGDVAA 96
Db 343 GVQFTTKVRLLVKFPPELNYQLKVCIDKESGDVAA 378

RESULT 15
Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FPE18BEFD8BE CRC64;

Query Match          93.3%; Score 461; DB 2; Length 764;
Best Local Similarity 91.7%; Pred. No. 3.5e-42;
Matches 88; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLEELQKQVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 60
Db 283 KLEELQKQVSYKGDPIVQHRPMLERIVELFNLKMSAFVVERQPCMPMHPDRPLVIKT 342

Qy 61 GVQFTTKVRLLVKFPPELNYQLKVCIDKDSGDVAA 96
Db 343 GVQFTTKVRLLVKFPPELNYQLKVCIDKESGDVAA 378

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Search completed: May 25, 2005, 17:43:42
Job time : 40.9444 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:14:45 ; Search time 121.891 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-29
Perfect score: 1169
Sequence: 1 NHPTAAVTEKQOMLEOHLQ.....IKTGVPATAVALLVKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003Bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1160	99.2	229	AA72860	Aay72860 Mouse Sta
2	1155	98.8	229	AA72850	Aay72850 Mouse Sta
3	1155	98.8	252	AA72846	Aay72846 Mouse Sta
4	1155	98.8	271	AA72841	Aay72841 Mouse Sta
5	1155	98.8	770	AA72082	Aay72082 Mouse Sta
6	1155	98.8	770	AAW03176	Aaw03176 Mouse Sta
7	1151	98.5	229	AA72863	Aay72863 Mouse Sta
8	1150	98.4	229	AA72862	Aay72862 Mouse Sta
9	1144	97.9	720	AAE22055	Aae22055 Human Sta
10	1144	97.9	769	ABBS7164	Abb57164 Mouse isc
11	1144	97.9	769	AAE22054	Aae22054 Human Sta
12	1144	97.9	769	AAE22056	Aae22056 Human pro
13	1144	97.9	770	AAE22055	Aae22055 Mouse liv
14	1144	97.9	770	AA703768	Aay03768 Human STA
15	1144	97.9	770	AA712377	Aab12377 N-termina
16	1144	97.9	770	AAE14652	Aae14652 Murine ST
17	1144	97.9	770	ABG69497	Abg69497 Human bai
18	1144	97.9	770	ABU10476	Abu10476 Mouse Sta
19	1144	97.9	770	ADN04365	Adn04365 Antipsori
20	1144	97.9	770	ADP54789	Adp54789 Human PRO
21	1144	97.9	793	AAAB58442	Aab58442 Lung canc
22	1141	97.6	770	ADDA4738	Add44738 Rat Prote
23	1140.5	97.6	228	AA72861	Aay72861 Mouse Sta
24	1139	97.4	770	AAE22993	Aae22993 Human pia
25	1139	97.4	770	AAE19964	Aae19964 Human sig

26	1139	97.4	770	5	AAE15174	Aae15174 Human Sta
27	1139	97.4	770	7	ADD44740	Add44740 Human Pro
28	1094	93.6	213	4	AA72851	Aay72851 Mouse Sta
29	1094	93.6	236	4	AA72847	Aay72847 Mouse Sta
30	1027	87.9	223	4	AA72854	Aay72854 Mouse Sta
31	828	70.8	185	4	AA72855	Aay72855 Mouse Sta
32	781	66.8	176	4	AA72848	Aay72848 Mouse Sta
33	653	55.9	128	4	AA72852	Aay72852 Mouse Sta
34	605	51.8	143	4	AA72849	Aay72849 Mouse Sta
35	560	47.9	749	5	AA78526	Aag78526 Rat STAT-
36	556	47.6	268	4	AA72844	Aay72844 Mouse Sta
37	556	47.6	582	2	AAW62996	Aaw62996 Human tru
38	556	47.6	582	6	ABU04748	Abu04748 Human exp
39	556	47.6	582	8	ADH57036	Adh57036 Truncated
40	556	47.6	680	6	ABR59713	Abr59713 Human sig
41	556	47.6	712	2	AA72079	Aar72079 Human sig
42	556	47.6	712	2	AAW03170	Aaw03170 Human STA
43	556	47.6	712	2	AAW62995	Aaw62995 Human Sta
44	556	47.6	712	6	ABU04747	Abu04747 Human exp
45	556	47.6	712	6	ABU04735	Abu04735 Human exp

ALIGNMENTS

RESULT 1
AA72860
ID AAY72860 standard; protein; 229 AA.
XX AC AAY72860;
XX DT 31-MAY-2001 (first entry)
XX DE Mouse Stat3 mutant (L148A,V151A,T346A,K348A,R350A) protein fragment.
XX KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy; mutant; mutein.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
FT Region 1..25
FT /note= "Stat3-c-Jun interaction region 1; corresponds to 130-154 position of Stat3 protein"
FT Misc-difference 19
FT /note= "Wild type Leu substituted with Ala; corresponds to 148 position of Stat-3 protein"
FT Misc-difference 22
FT /note= "Wild type Val substituted with Ala corresponds to 151 position of Stat-3 protein"
FT Region 213..229
FT /note= "Stat3-c-Jun interaction region 2; corresponds to 342-358 position of Stat3 protein"
FT Misc-difference 217
FT /note= "Wild type Thr substituted with Ala corresponds to 346 position of Stat-3 protein"
FT Misc-difference 219
FT /note= "Wild type Lys substituted with Ala corresponds to 348 position of Stat-3 protein"
FT Misc-difference 221
FT /note= "Wild type Arg substituted with Ala corresponds to 350 position of Stat-3 protein"
XX WO200116605-A2.
XX 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023822.
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
PA

XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JB;
XX WPI; 2001-226705/23.
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX Example 4; Page; 86pp; English.
XX The present sequence is mouse Stat3 mutant protein fragment containing
XX 130-358 amino acids of Stat3 protein. This mutant is obtained by
XX replacing Leu 148 with Ala, Val 151 with Ala, Thr 346 with Ala, Lys 348
XX with Ala and Arg 350 with Ala in the Stat3 protein. The invention relates
XX to methods for identifying interacting regions of transcription factors
XX and methods for identifying agents which modulates the interaction
XX between a transcription factor such as c-Jun and a Stat protein such as
XX Stat-1 and Stat-3, useful for modulating gene transcription e.g.,
XX cellular transformation. These identifying agents are used in the
XX treatment of dysproliferative diseases and also for treating cancer and
XX psoriasis. A Stat protein comprises the N-terminal domain, coiled-coil
XX domain, DNA binding domain, linker domain, SH2 domain and transactivation
XX domain
XX Sequence 229 AA;
Query Match 99.2%; Score 1160; DB 4; Length 229;
Best Local Similarity 99.1%; Pred. No. 1.5e-98;
Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 NHPTAAVVTKEQMLQHLQDVRRKRVQDLQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 60
Db 1 NHPTAAVVTKEQMLQHLQHAQDKRKVDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 60
Qy 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Qy 121 ACIGGPNICLDRLNWIITSLAESQLQTRQIQKLELQKQVSKGDPVQHRPMLERI 180
Db 121 ACIGGPNICLDRLNWIITSLAESQLQTRQIQKLELQKQVSKGDPVQHRPMLERI 180
Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 229
Db 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 229
RESULT 2
AA72850
ID AAY72850 standard; protein; 229 AA.
XX AAY72850;
XX AC AAY72850;
XX DT 31-MAY-2001 (first entry)
XX DE Mouse Stat3 protein fragment #8 (130-358 amino acids).
XX KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
XX KW cellular transformation; dysproliferative disease; cancer; psoriasis;
XX KW therapy.
XX OS Mus musculus.
XX PH Key Location/Qualifiers
XX FT Region 1. .25
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
FT Region 213. .229
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX WO200116605-A2.
XX PN
XX

PD 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023822.
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JB;
XX WPI; 2001-226705/23.
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX Claim 65; Page 76-77; 86pp; English.
XX The present sequence is mouse Stat3 protein fragment containing 130-358
XX amino acids of Stat3 protein. This Stat3 fragment showed strong binding
XX to c-Jun protein in the cell extract. The invention relates to methods
XX for identifying interacting regions of transcription factors and methods
XX for identifying agents which modulates the interaction between a
XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
XX Stat-3, useful for modulating gene transcription e.g., cellular
XX transformation. These identifying agents are used in the treatment of
XX dysproliferative diseases and also for treating cancer and psoriasis. A
XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
XX binding domain, linker domain, SH2 domain and transactivation domain
XX Sequence 229 AA;
Query Match 98.8%; Score 1155; DB 4; Length 229;
Best Local Similarity 98.7%; Pred. No. 4.4e-98;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 NHPTAAVVTKEQMLQHLQDVRRKRVQDLQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 60
Db 1 NHPTAAVVTKEQMLQHLQDVRRKRVQDLQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 60
Qy 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Qy 121 ACIGGPNICLDRLNWIITSLAESQLQTRQIQKLELQKQVSKGDPVQHRPMLERI 180
Db 121 ACIGGPNICLDRLNWIITSLAESQLQTRQIQKLELQKQVSKGDPVQHRPMLERI 180
Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 229
Db 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 229
RESULT 3
AA72846
ID AAY72846 standard; protein; 252 AA.
XX AAY72846;
XX AC AAY72846;
XX DT 31-MAY-2001 (first entry)
XX DE Mouse Stat3 protein fragment #4 (107-358 amino acids).
XX KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
XX KW cellular transformation; dysproliferative disease; cancer; psoriasis;
XX KW therapy.
XX OS Mus musculus.
XX PH Key Location/Qualifiers
XX FT Region 24. .48
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
FT Region 236. .252
FT

FT FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 XX FT 342-358 position of Stat3 protein"
 PN WO200116605-A2.
 XX 08-MAR-2001.
 PD 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 PF (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX Claim 65; Page 73; 86pp; English.
 XX The present sequence is mouse Stat3 protein fragment containing 107-358
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX Sequence 252 AA;
 SQ
 Query Match 98.8%; Score 1155; DB 4; Length 252;
 Best Local Similarity 98.7%; Pred. No. 5e-98;
 Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHLQDVRRVQDLEQKMKVVENLODDFDNFYKTLKSGQDMQDLN 60
 DB 24 NHPTAAVVTKEQOMLEQHLQDVRRVQDLEQKMKVVENLODDFDNFYKTLKSGQDMQDLN 83
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 84 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
 DB 144 ACIGGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 203
 QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFATAVALLVKPEL 229
 DB 204 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFATAVALLVKPEL 252
 RESULT 4
 AAY72841
 ID AAY72841 standard; protein; 271 AA.
 XX AAY72841;
 XX 31-MAY-2001 (first entry)
 XX Mouse Stat3 protein fragment #2 (107-377 amino acids).
 DE Mouse; Stat3 protein; transcription factor; c-Jun; Gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX Mus musculus.
 OS
 XX

FH Key Location/Qualifiers
 FT Region 24..48
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT 236..252
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX WO200116605-A2.
 PN 08-MAR-2001.
 PD 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 PR (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX Claim 65; Page 67-68; 86pp; English.
 XX The present sequence is mouse Stat3 protein fragment containing 107-377
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX Sequence 271 AA;
 SQ
 Query Match 98.8%; Score 1155; DB 4; Length 271;
 Best Local Similarity 98.7%; Pred. No. 5.5e-98;
 Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHLQDVRRVQDLEQKMKVVENLODDFDNFYKTLKSGQDMQDLN 60
 DB 24 NHPTAAVVTKEQOMLEQHLQDVRRVQDLEQKMKVVENLODDFDNFYKTLKSGQDMQDLN 83
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 84 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
 DB 144 ACIGGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 203
 QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFATAVALLVKPEL 229
 DB 204 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFATAVALLVKPEL 252
 RESULT 5
 AAR72082
 ID AAR72082 standard; protein; 770 AA.
 XX AAR72082;
 XX 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX Mouse Stat3 (19sf6).
 DE
 XX

KW Signal transducer and activator of transcription; STAT3; 19sf6; Stat3;
 KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
 KW derangement; dysfunction; interferon-gamma.
 XX

OS Mus sp.
 XX
 XX WO9508629-A1.
 XX
 XX 30-MAR-1995.
 XX
 XX 26-SEP-1994; 94WO-US010849.
 XX
 XX 24-SEP-1993; 93US-00126588.
 XX
 XX 24-SEP-1993; 93US-00126595.
 XX
 XX 11-MAR-1994; 94US-00212184.
 XX
 XX 11-MAR-1994; 94US-00212185.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 XX
 XX WPI; 1995-139598/18.
 XX
 XX N-PSDB; AAQ89340.
 XX

Receptor recognition factor implicated in transcriptional stimulation of
 genes - useful in drug screening assays and/or for treating cellular
 debilitations, derangements and/or dysfunctions, etc.

XX Claim 1; Page 107-110; 160pp; English.

XX A fragment encoding the human Stat91 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
 CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC -40) were cloned in plasmids 13sf1 and 19sf6 and encoded proteins termed
 CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX

SQ Sequence 770 AA;

Query Match 98.8%; Score 1155; DB 2; Length 770;
 Best Local Similarity 98.7%; Pred. No. 2.2e-97;
 Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NHPTAAVVTKEQQMLQHLQDVVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGMQDLN 60
 Db 130 NHPTAAVVTKEQQMLQHLQDVVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGMQDLN 189
 Qy 61 GNNQSVTRQKMQQLQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQQLQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDEELADWKRRPEI 249
 Qy 121 ACIGGPPNICLDRLNWTSLAESQLQTRQIQIKLELQKVSYKGDPIVQHRPMLERI 180
 Db 250 ACIGGPPNICLDRLNWTSLAESQLQTRQIQIKLELQKVSYKGDPIVQHRPMLERI 309
 Qy 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKFPPEL 229
 Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKFPPEL 358

RESULT 6
 AA03176
 ID AA03176 standard; protein; 770 AA.
 XX

XX AA03176;
 XX AC
 XX 24-OCT-1996 (first entry)
 XX
 XX Mouse STAT4.
 DE
 XX

KW STAT; STAT4; signal transducer and activator of transcription;
 KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
 KW autoimmune disease; antagonist; therapy.
 XX

OS Mus sp.
 XX
 XX Location/Qualifiers
 XX Key 398..508
 XX Domain /label= DNA binding domain
 XX /note= "Claim 3, page 110"
 XX
 XX WO9620954-A2.
 XX
 XX 11-JUL-1996.
 XX
 XX 28-DEC-1995; 95WO-US017025.
 XX
 XX 06-JAN-1995; 95US-00369796.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Darnell JE, Wen Z, Horvath CM, Zhong Z;
 XX
 XX WPI; 1996-333941/33.
 XX
 XX N-PSDB; AAT31280.
 XX

New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,
 preventing or treating cellular dysfunction, e.g. oncogenesis,
 PT inflammation, parasitic disease or autoimmunity.

XX Disclosure; Page 87-90; 138pp; English.

XX Mouse signal transducer and activator of transcription (STAT) protein
 CC STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from
 CC ligand-activated receptor kinase complexes followed by nuclear
 CC translocation and DNA binding to activate transcription. Recombinant
 CC STAT4 can be obtd. using cDNA clone 19sf6 (AAT31278) obtd. from
 CC splenic/thymic cells. STAT4 includes a DNA-binding domain (see also
 CC AA03167) capable of both receptor recognition and message delivery via
 CC DNA binding in a receptor-ligand specific manner. STAT proteins and their
 CC DNA binding domains (see also AA03165-75) are useful for screening
 CC antagonists used to inhibit STAT-mediated signal transduction and
 CC activation of transcription

XX Sequence 770 AA;

Query Match 98.8%; Score 1155; DB 2; Length 770;
 Best Local Similarity 98.7%; Pred. No. 2.2e-97;
 Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NHPTAAVVTKEQQMLQHLQDVVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGMQDLN 60
 Db 130 NHPTAAVVTKEQQMLQHLQDVVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGMQDLN 189
 Qy 61 GNNQSVTRQKMQQLQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQQLQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDEELADWKRRPEI 249
 Qy 121 ACIGGPPNICLDRLNWTSLAESQLQTRQIQIKLELQKVSYKGDPIVQHRPMLERI 180
 Db 250 ACIGGPPNICLDRLNWTSLAESQLQTRQIQIKLELQKVSYKGDPIVQHRPMLERI 309
 Qy 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKFPPEL 229
 Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKFPPEL 358

RESULT 7
 AA03176
 ID AA03176 standard; protein; 770 AA.
 XX

XX AA03176;
 XX AC
 XX 24-OCT-1996 (first entry)
 XX
 XX Mouse STAT4.
 DE
 XX

DT 31-MAY-2001 (first entry)
 DE Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutin.
 XX
 OS Mus musculus.
 XX
 XX Key Location/Qualifiers
 FH Region 1. .25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Misc-difference 22
 FT /note= "Wild type Val substituted with Ala corresponds to
 FT 151 position of Stat-3 protein"
 FT Region 213. .229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 XX 08-MAR-2001.
 XX
 XX 30-AUG-2000; 2000WO-US023822.
 PF
 XX 31-AUG-1999; 99US-00387418.
 PR
 XX (UYRQ) UNIV ROCKEFELLER.
 PA
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 PI WPI; 2001-226705/23.
 XX
 DR Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 PT
 XX Claim 66; Page 86; 86pp; English.
 PS
 XX The present sequence is mouse Stat3 mutant (V151A) protein fragment
 CC containing 130-358 amino acids of Stat3 protein. This mutant is obtained
 CC by replacing Val 151 with Ala in Stat3 protein. The invention relates to
 CC methods for identifying interacting regions of transcription factors and
 CC methods for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 229 AA;
 Query Match 98.5%; Score 1151; DB 4; Length 229;
 Best Local Similarity 98.3%; Pred. No. 1e-97;
 Matches 225; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQKQMLQHLQDVRRKRVODLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 DB 1 NHPTAAVVTKEQKQMLQHLQDARRRVODLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 QY 61 GNNQSVTRQKMQQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 DB 61 GNNQSVTRQKMQQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 QY 121 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEELQKQVYKGDPIVQHRPMLERI 180
 DB 121 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEELQKQVYKGDPIVQHRPMLERI 180
 QY 181 VELFRNLMSAFVVERQPCMPHPDRPLVIKTGVQFATAVALLVKKPEL 229
 DB 181 VELFRNLMSAFVVERQPCMPHPDRPLVIKTGVQFATAVALLVKKPEL 229

RESULT 8
 AAY72862
 ID AAY72862 standard; protein; 229 AA.
 XX
 AC AAY72862;
 XX
 XX 31-MAY-2001 (first entry)
 XX
 XX Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).
 DE
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutin.
 XX
 OS Mus musculus.
 XX
 XX Key Location/Qualifiers
 FH Region 1. .25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Misc-difference 19
 FT /note= "Wild type Leu substituted with Ala; corresponds
 FT to 148 position of Stat-3 protein"
 FT Region 213. .229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 XX 08-MAR-2001.
 XX
 XX 30-AUG-2000; 2000WO-US023822.
 PF
 XX 31-AUG-1999; 99US-00387418.
 PR
 XX (UYRQ) UNIV ROCKEFELLER.
 PA
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 PI WPI; 2001-226705/23.
 XX
 DR Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 PT
 XX Claim 66; Page 85; 86pp; English.
 PS
 XX The present sequence is mouse Stat3 mutant (L148A) protein fragment
 CC containing 130-358 amino acids of Stat3 protein. This mutant is obtained
 CC by replacing Leu 148 with Ala in Stat3 protein. The invention relates to
 CC methods for identifying interacting regions of transcription factors and
 CC methods for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 229 AA;
 Query Match 98.4%; Score 1150; DB 4; Length 229;
 Best Local Similarity 98.3%; Pred. No. 1.3e-97;
 Matches 225; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQKQMLQHLQDVRRKRVODLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 DB 1 NHPTAAVVTKEQKQMLQHLQDARRRVODLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 QY 61 GNNQSVTRQKMQQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 DB 61 GNNQSVTRQKMQQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

QY 121 ACIGPPNICLDRLNWIITSLAESOLQTRQIKLEELQKQVSKGDPVIOHRPMLERI 180
 DB 121 ACIGPPNICLDRLNWIITSLAESOLQTRQIKLEELQKQVSKGDPVIOHRPMLERI 180
 QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVITKGVQFATAVALLVKFPPEL 229
 DB 181 VELFRNLKMSAFVVERQPCMPHDPRLVITKGVQFATAVALLVKFPPEL 229

RESULT 9

AAE22055
 ID AAE22055 standard; protein; 720 AA.

AC AAE22055;

DT 25-JUL-2002 (first entry)

XX Human Stat3beta protein.

XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW shock; chronic active hepatitis; emphysema; trauma; scleroderma;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion; Statbeta.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 713..714
 FT /note= "Encoded by ACA CCA TTC"

PN WO200220032-A1.

XX 14-MAR-2002.

XX 10-SEP-2001; 2001WO-US028254.

XX 08-SEP-2000; 2000US-0231212P.

XX (UYJO) UNIV JOHNS HOPKINS.

XX (UYSF-) UNIV SOUTH FLORIDA.

XX Yu H, Pardoll D, Jove R, Dalton W;

XX WPI; 2002-362218/39.

XX N-PSDB; AAD35066.

XX Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.

XX Disclosure; Page 87-89; 94pp; English.

XX The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy

CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC Stat3beta protein
 XX

SQ Sequence 720 AA;

Query Match 97.9%; Score 1144; DB 5; Length 720;

Best Local Similarity 97.8%; Pred. No. 2e-96;

Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQKQMLEQHLQDVVKRVQDLEQKMKVVENLQDDPFDNYKTLKSQDMDLN 60

DB 130 NHPTAAVVTKEQKQMLEQHLQDVVKRVQDLEQKMKVVENLQDDPFDNYKTLKSQDMDLN 189

QY 61 GNNQSVTRQKMQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

DB 190 GNNQSVTRQKMQLEQMLTALDQRRRSIVSELAGLLSAMEYVQKTLTDEELADWKRQOI 249

QY 121 ACIGPPNICLDRLNWIITSLAESOLQTRQIKLEELQKQVSKGDPVIOHRPMLERI 180

DB 250 ACIGPPNICLDRLNWIITSLAESOLQTRQIKLEELQKQVSKGDPVIOHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVITKGVQFATAVALLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVITKGVQFATAVALLVKFPPEL 358

RESULT 10

ABB57164

ID ABB57164 standard; protein; 769 AA.

AC ABB57164;

XX 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related protein sequence SEQ ID NO:398.

XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

XX vasospastic ischaemia; ischaemic condition; ischaemic disease.

XX Mus musculus.

XX WO2001188188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-JP004192.

XX 18-MAY-2000; 2000JP-00145977.

XX (UYNT-) UNIV NIHOON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.

XX N-PSDB; ABI99454.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by

PT determining the expression profile of a gene group comprising these
 XX genes.

Claim 2; Page 1084-1087; 2690pp; English.

CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (1) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (1). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI999202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention

XX Sequence 769 AA;

Query Match 97.9%; Score 1144; DB 5; Length 769;
 Best Local Similarity 97.8%; Pred. No. 2.2e-96;
 Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQOMLEQHLQDVKRVRQVQDLKQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 60
 Db 130 NHPTAAVTEKQOMLEQHLQDVKRVRQVQDLKQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQKMOQLEOMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDELDADWKRPEI 120
 Db 190 GNNQSVTRQKMOQLEOMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDELDADWKRPEI 249
 QY 121 ACIGGPPNCLDRLENWITSLAESQLOTRQIQKLELQKQVSKYKGDPIVQHRPMLERI 180
 Db 250 ACIGGPPNCLDRLENWITSLAESQLOTRQIQKLELQKQVSKYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 229
 Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 358

RESULT 11
 AAE22054
 ID AAE22054 standard; protein; 769 AA.
 XX
 AC AAE22054;

25-JUL-2002 (first entry)

Human Stat3 protein.

XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.

XX Homo sapiens.

OS WO200220032-A1.

PN 14-MAR-2002.

PD 10-SEP-2001; 2001WO-US028254.

XX

PR 08-SEP-2000; 2000US-0231212P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (UYSF-) UNIV SOUTH FLORIDA.

XX Yu H, Pardoll D, Jove R, Dalton W;

XX WPI; 2002-362218/39.
 DR N-PSDB; AAD35065.

PT Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.

XX Disclosure; Page 83-85; 94pp; English.

XX The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g.; bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human Stat3
 CC protein

XX Sequence 769 AA;

Query Match 97.9%; Score 1144; DB 5; Length 769;
 Best Local Similarity 97.8%; Pred. No. 2.2e-96;
 Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVKRVRQVQDLKQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 60
 Db 130 NHPTAAVTEKQOMLEQHLQDVKRVRQVQDLKQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQKMOQLEOMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDELDADWKRPEI 120
 Db 190 GNNQSVTRQKMOQLEOMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDELDADWKRPEI 249
 QY 121 ACIGGPPNCLDRLENWITSLAESQLOTRQIQKLELQKQVSKYKGDPIVQHRPMLERI 180
 Db 250 ACIGGPPNCLDRLENWITSLAESQLOTRQIQKLELQKQVSKYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 229
 Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 358

RESULT 12
 AAE22056
 ID AAE22056 standard; protein; 769 AA.

XX AC AAE22056;
 XX KW Human protein related to angiogenesis regulation.
 XX DT 25-JUL-2002 (first entry)
 XX DE
 XX KW Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW Sjogren's syndrome; proliferative angiopathy; autoimmune thyroiditis;
 KW nitrogen necrosis; multiple sclerosis; Addison's disease; epilepsy;
 KW polyomyelitis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.
 XX OS Homo sapiens.
 XX KW WO200220032-A1.
 XX PN 14-MAR-2002.
 XX FD 10-SEP-2001; 2001WO-US028254.
 XX PF 08-SEP-2000; 2000US-0231212P.
 XX PR (UYJO) UNIV JOHNS HOPKINS.
 XX PA (UYSF-) UNIV SOUTH FLORIDA.
 XX KW Yu H, Pardoll D, Jove R, Dalton W;
 XX WPI; 2002-362218/39.
 XX DR
 XX PT Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.
 XX PS Disclosure; Page 83-85; 94pp; English.
 XX CC The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC protein related to angiogenesis regulation

SQ Sequence 769 AA;
 Query Match 97.9%; Score 1144; DB 5; Length 769;
 Best Local Similarity 97.8%; Pred. No. 2.2e-96;
 Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQOMLEHQLQDVVRKRVODLEQRMKVVENLQDDFDNFYKTLKSGDMQDLN 60
 DB 130 NHPTAAVTEKQOMLEHQLQDVVRKRVODLEQRMKVVENLQDDFDNFYKTLKSGDMQDLN 189
 QY 61 GNNQSVTRQKMOOLEOMLTALDQRRSIVSELAGLISAMEYVQKTLTDEELADMKRPEI 120
 DB 190 GNNQSVTRQKMOOLEOMLTALDQRRSIVSELAGLISAMEYVQKTLTDEELADMKRQOI 249
 QY 121 ACIGGPPNICLDLENWITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVOHRPMLERI 180
 DB 250 ACIGGPPNICLDLENWITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVOHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKPPPEL 229
 DB 310 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKPPPEL 358
 RESULT 13
 AAR82995
 ID AAR82995 standard; protein; 770 AA.
 AC AAR82995;
 XX 25-MAR-1996 (first entry)
 DT Mouse liver acute phase response factor.
 DE Mouse; acute phase response factor; transcription factor; interleukin-6;
 KW signal transduction; liver; antibody; antisease; ribozyme;
 KW antiinflammatory; antitumor; hypotensive; therapy.
 XX OS Mus musculus.
 XX PN EP676469-A2.
 XX PD 11-OCT-1995.
 XX PF 29-MAR-1995; 95EP-00104670.
 XX PR 04-APR-1994; 94JP-00065825.
 XX PA (KISH/) KISHIMOTO T.
 XX PI Akira S, Kishimoto T;
 XX WPI; 1995-346089/45.
 XX N-PSDB; AAT05619.
 XX PT New acute phase response factor - for developing inhibitory agents for
 PT treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
 PT diseases.
 XX PS Claim 10; Page 20-22; 31pp; English.
 XX CC The sequence represents a mouse acute phase response factor (APRF), a
 CC transcription factor related to signal transduction of interleukin-6 (IL-
 CC 6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
 CC library using a polymerase chain reaction product (amplified using
 CC primers derived from an IL-6-treated mouse liver peptide) as a probe.
 CC APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
 CC ribozymes, may be used to treat diseases induced by IL-6, e.g.
 CC inflammatory disease, leukemia, cancer, osteoclastia, pulmonary
 CC hypertension, etc
 XX SQ Sequence 770 AA;
 Query Match 97.9%; Score 1144; DB 2; Length 770;

Best Local Similarity 97.8%; Pred. No. 2.2e-96;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQMLQHLQDVRRKRVQDLQEQMKVVENLQDDFDFNYKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQMLQHLQDVRRKRVQDLQEQMKVVENLQDDFDFNYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKQWQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKQWQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQOI 249

QY 121 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLELQKVS YKGDPIVQHRPMLBERI 180
DB 250 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLELQKVS YKGDPIVQHRPMLBERI 309

QY 181 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 229
DB 310 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 358

RESULT 14
AAY03768
ID AAY03768 standard; protein; 770 AA.
XX
AC AAY03768;
XX
DT 11-JUN-1999 (first entry)
XX
DE Human STAT3 allelic variant.
XX
KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;
KW intracellular transcription factor; interleukin-6; medicament; variant;
KW pharmaceutical; autoimmune disease; inflammatory; human.
XX
OS Homo sapiens.
XX
PN EP905234-A2.
XX
PD 31-MAR-1999.
XX
PF 18-FEB-1998; 98EP-00102774.
XX
PR 16-SEP-1997; 97EP-00116061.
XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Serlupi-Crescenzi O, Della Pietra L;
XX
DR WPI; 1999-192664/17.
XX
DR N-PSDB; AAX29281.
XX
PT New human Signal Transducer and Activator of Transcription 3 (STAT3)
PT allelic variant useful for treatment of autoimmune and inflammatory
PT disease.
XX
PS Claim 2; Page 9-13; 32pp; English.
XX
CC The present sequence represents a predominant allelic variant of human
CC Signal Transducer and Activator of Transcription 3 (STAT3) protein, an
CC intracellular transcription factor which mediates IL-6 signals. The
CC encoding sequence differs from the original published human STAT3 gene
CC sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3
CC DNA molecule can be used for the recombinant expression of the variant.
CC STAT3 protein is useful as a medicament or pharmaceutical composition for
CC treatment of autoimmune or inflammatory diseases
XX
SQ Sequence 770 AA;

Query Match 97.9%; Score 1144; DB 2; Length 770;
Best Local Similarity 97.8%; Pred. No. 2.2e-96;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQMLQHLQDVRRKRVQDLQEQMKVVENLQDDFDFNYKTLKSGQDMQDLN 60

DB 130 NHPTAAVVTKEQMLQHLQDVRRKRVQDLQEQMKVVENLQDDFDFNYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKQWQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKQWQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQOI 249

QY 121 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLELQKVS YKGDPIVQHRPMLBERI 180
DB 250 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLELQKVS YKGDPIVQHRPMLBERI 309

QY 181 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 229
DB 310 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL 358

RESULT 15
AAB12377
ID AAB12377 standard; peptide; 770 AA.
XX
AC AAB12377;
XX
DT 08-NOV-2000 (first entry)
XX
DE N-terminal domain of murine STAT-3 protein.
XX
KW STAT; signal transducer and activator of transcription; crystal;
KW drug design; murine.
XX
OS Mus sp.
XX
FH Key
FH Region 4..9
FT /label= Alpha helix 1
FT Region 12..21
FT /label= Alpha helix 2
FT Region 19..21
FT /label= 3(10) helix of alpha helix 2
FT Region 28..33
FT /label= Alpha helix 3
FT Region 35..40
FT /label= Alpha helix 4
FT Region 43..47
FT /label= Alpha helix 5
FT Region 50..73
FT /label= Alpha helix 6
FT Region 77..96
FT /label= Alpha helix 7
FT Region 99..119
FT /label= Alpha helix 8
XX
PN US6087478-A.
XX
PD 11-JUL-2000.
XX
PF 23-JAN-1998; 98US-00012710.
XX
PR 23-JAN-1998; 98US-00012710.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;
XX
DR WPI; 2000-505108/45.
XX
PT New crystals of an N-terminal fragment of a signal transducer and
PT activator of transcription that effectively diffracts x-rays, useful for
PT drug screening and development.
XX
PS Disclosure; Fig 1; 42pp; English.
XX
CC The present invention relates to a crystal of an N-terminal fragment of a
CC signal transducer and activator of transcription (STAT) protein. The

CC crystal effectively diffracts X-rays, allowing the determination of the
CC atomic coordinates of the N-terminal domain to a resolution of greater
CC than 5.0 Angstroms. The present sequence is the N-terminal domain of the
CC murine STAT 3 protein. The N-terminal domain enables STAT dimers to
CC interact and bind DNA cooperatively, a mechanism important for gene
CC activation. The crystals are useful in drug screening and development by
CC selecting a potential drug by performing rational drug design with the 3-
CC dimensional structure determined for the crystal
XX
SQ Sequence 770 AA;

Query Match	97.9%;	Score 1144;	DB 3;	Length 770;
Best Local Similarity	97.8%;	Pred. No. 2.2e-96;		
Matches 224;	Conservative 1;	Mismatches 4;	Indels 0;	Gaps 0;

Qy	1	NHPTAAVVTKEQQMLEOHLQDVVRKRVQDLFOKMKVVENLQDDFDNFNYKTLKSQGDMDLN	60
Db	130	NHPTAAVVTKEQQMLEOHLQDVVRKRVQDLFOKMKVVENLQDDFDNFNYKTLKSQGDMDLN	189
Qy	61	GNNQSVTRQKMQQLEQMLTALDDMRRTIVSELAGLLSAMEYVQKTLTDEELADWKREPEI	120
Db	190	GNNQSVTRQKMQQLEQMLTALDDMRRTIVSELAGLLSAMEYVQKTLTDEELADWKRRQOI	249
Qy	121	ACIGPPNICLDRLNNWITSLSAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLLEERI	180
Db	250	ACIGPPNICLDRLNNWITSLSAESQLQTRQIKKLEELQOKVSYKGDPIVQHRPMLLEERI	309
Qy	181	VELFRNLKSAFVVERQPCMPMPDRPLVKTGVQFATAVALLVKFPPEL	229
Db	310	VELFRNLKSAFVVERQPCMPMPDRPLVKTGVQFATAVALLVKFPPEL	358

Search completed: May 25, 2005, 17:36:37
Job time : 123.057 secs

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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 28.6534 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-29
Perfect score: 1169
Sequence: 1 NHPTAAVTEKQOMLEQHQLQ.....IKTGQFATAVALLVKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCUTS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1155	98.8	229	3	US-09-387-418A-18
3	1155	98.8	229	3	US-09-387-418A-28
4	1155	98.8	252	3	US-09-387-418A-14
5	1155	98.8	271	3	US-09-387-418A-9
6	1155	98.8	770	1	US-08-369-796-12
7	1155	98.8	770	2	US-08-852-091-12
8	1155	98.8	770	2	US-08-820-754-12
9	1155	98.8	770	3	US-08-956-652-12
10	1155	98.8	770	3	US-08-956-869-12
11	1155	98.8	770	3	US-08-948-547-12
12	1155	98.8	770	3	US-09-364-970-3
13	1155	98.8	770	3	US-09-364-970-5
14	1155	98.8	770	3	US-08-956-653A-12
15	1155	98.8	770	4	US-08-212-185-12
16	1155	98.8	770	5	PCT-US95-17025-12
17	1151	98.5	229	3	US-09-387-418A-31
18	1150	98.4	229	3	US-09-387-418A-30
19	1144	97.9	770	1	US-08-416-581B-9
20	1144	97.9	770	3	US-09-012-710-8
21	1144	97.9	770	3	US-09-556-273-8
22	1144	97.9	770	3	US-09-526-542-2
23	1144	97.9	770	4	US-10-117-087-2
24	1139	97.4	770	1	US-08-416-581B-1
25	1139	97.4	770	1	US-08-416-581B-5
26	1139	97.4	770	3	US-09-087-465-6
27	1139	97.4	770	4	US-09-972-800A-6

28	1139	97.4	771	1	US-08-276-099A-14	Sequence 14, Appl
29	1139	97.4	771	1	US-08-781-890-14	Sequence 14, Appl
30	1094	93.6	213	3	US-09-387-418A-19	Sequence 19, Appl
31	1094	93.6	236	3	US-09-387-418A-15	Sequence 15, Appl
32	1027	87.9	223	3	US-09-387-418A-22	Sequence 22, Appl
33	828	70.8	185	3	US-09-387-418A-23	Sequence 23, Appl
34	781	66.8	176	3	US-09-387-418A-16	Sequence 16, Appl
35	653	55.9	128	3	US-09-387-418A-20	Sequence 20, Appl
36	605	51.8	143	3	US-09-387-418A-17	Sequence 17, Appl
37	556	47.6	268	3	US-09-387-418A-12	Sequence 12, Appl
38	556	47.6	582	4	US-09-430-806A-3	Sequence 3, Appl
39	556	47.6	712	1	US-08-369-796-6	Sequence 6, Appl
40	556	47.6	712	2	US-08-852-091-6	Sequence 6, Appl
41	556	47.6	712	2	US-08-820-754-6	Sequence 6, Appl
42	556	47.6	712	3	US-08-956-652-6	Sequence 6, Appl
43	556	47.6	712	3	US-08-956-869-6	Sequence 6, Appl
44	556	47.6	712	3	US-08-948-547-6	Sequence 6, Appl
45	556	47.6	712	3	US-08-956-653A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-387-418A-29
; Sequence 29, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 29
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-29

Query Match		100.0%;	Score 1169;	DB 3;	Length 229;
Best Local Similarity		100.0%;	Pred No. 4e-99;		
Matches 229;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	NHPTAAVTEKQOMLEQHQLQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN	60		
DB	1	NHPTAAVTEKQOMLEQHQLQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN	60		
QY	61	GNNQSVTRQKMOQLEMTALDOMRSIVSELAGLLSAMEYVQKTTTDEELADMKRPEI	120		
DB	61	GNNQSVTRQKMOQLEMTALDOMRSIVSELAGLLSAMEYVQKTTTDEELADMKRPEI	120		
QY	121	ACIGGPNICLDRLENWITSLAESQLQTRQIQKLEELQKYSYKGDPIVQHRPMLERI	180		
DB	121	ACIGGPNICLDRLENWITSLAESQLQTRQIQKLEELQKYSYKGDPIVQHRPMLERI	180		
QY	181	VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL	229		
DB	181	VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPPEL	229		

RESULT 2
US-09-387-418A-18
; Sequence 18, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H

```
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-18

Query Match      98.8%; Score 1155; DB 3; Length 229;
Best Local Similarity 98.7%; Pred. No. 7.6e-98;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 NHPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVENLQDDPDFNFKTLKSGQDMQDLN 60
Db      1 NHPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVENLQDDPDFNFKTLKSGQDMQDLN 60

Qy      61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db      61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

Qy      121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
Db      121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180

Qy      181 VELFRNLKMSAFVVERQPCMPHDPRLPLVKTGVQFATAVALLVKRPPEL 229
Db      181 VELFRNLKMSAFVVERQPCMPHDPRLPLVKTGVQFATAVALLVKRPPEL 229

RESULT 3
US-09-387-418A-28
; Sequence 28, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-28

Query Match      98.8%; Score 1155; DB 3; Length 229;
Best Local Similarity 98.7%; Pred. No. 7.6e-98;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 NHPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVENLQDDPDFNFKTLKSGQDMQDLN 60
Db      1 NHPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVENLQDDPDFNFKTLKSGQDMQDLN 60

Qy      61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db      61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

Qy      121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
Db      121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180

Qy      181 VELFRNLKMSAFVVERQPCMPHDPRLPLVKTGVQFATAVALLVKRPPEL 229
Db      181 VELFRNLKMSAFVVERQPCMPHDPRLPLVKTGVQFATAVALLVKRPPEL 229

US-09-387-418A-28
; Sequence 28, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-28

Query Match      98.8%; Score 1155; DB 3; Length 229;
Best Local Similarity 98.7%; Pred. No. 7.6e-98;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 NHPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVENLQDDPDFNFKTLKSGQDMQDLN 60
Db      1 NHPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVENLQDDPDFNFKTLKSGQDMQDLN 60

Qy      61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db      61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

Qy      121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
Db      121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
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Qy      181 VELFRNLKMSAFVVERQPCMPHDPRLPLVKTGVQFATAVALLVKRPPEL 229
Db      181 VELFRNLKMSAFVVERQPCMPHDPRLPLVKTGVQFATAVALLVKRPPEL 229

RESULT 4
US-09-387-418A-14
; Sequence 14, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-14

Query Match      98.8%; Score 1155; DB 3; Length 252;
Best Local Similarity 98.7%; Pred. No. 8.6e-98;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 NHPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVENLQDDPDFNFKTLKSGQDMQDLN 60
Db      24 NHPTAAVVTKEQOMLEQHLQDVVRKRVODLEQKMKVVENLQDDPDFNFKTLKSGQDMQDLN 83

Qy      61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db      84 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143

Qy      121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 180
Db      144 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLELOOKVSYKGDPIVQHRPMLERI 203

Qy      181 VELFRNLKMSAFVVERQPCMPHDPRLPLVKTGVQFATAVALLVKRPPEL 229
Db      204 VELFRNLKMSAFVVERQPCMPHDPRLPLVKTGVQFATAVALLVKRPPEL 252

RESULT 5
US-09-387-418A-9
; Sequence 9, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-9

Query Match      98.8%; Score 1155; DB 3; Length 271;
Best Local Similarity 98.7%; Pred. No. 9.4e-98;
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Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 60
DB 24 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 83
QY 61 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKLTDTSELADWKRPEI 120
DB 84 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKLTDTSELADWKRPEI 143
QY 121 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 144 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 203
QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKPEL 229
DB 204 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKPEL 252

RESULT 6
US-08-369-796-12
; Sequence 12, Application US/08369796
; Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-369-796-12

Query Match 98.8%; Score 1155; DB 1; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 189
QY 61 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKLTDTSELADWKRPEI 120

DB 190 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKLTDTSELADWKRPEI 249
QY 121 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKPEL 229
DB 310 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLVKPEL 358

RESULT 7
US-08-852-091-12
; Sequence 12, Application US/08852091
; Patent No. 5883228
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,091
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-852-091-12

Query Match 98.8%; Score 1155; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 189
QY 61 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKLTDTSELADWKRPEI 120
DB 190 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKLTDTSELADWKRPEI 249
QY 121 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLENWITSLAESQLQTRQIQIKKLEELQKVS YKGDPIVQHRPMLERI 309

Qy 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVTKTGQFATAVALLVKFPPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVTKTGQFTTKVRLLVKFPPEL 358

RESULT 8

US-08-820-754-12
; Sequence 12, Application US/08820754
; Patent No. 5976835
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,754
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-754-12

Query Match 98.8%; Score 1155; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NHPTAAVVTKEQMLEQHLQDVRRKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 60
Db 130 NHPTAAVVTKEQMLEQHLQDVRRKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 189

Qy 61 GNNQSVTRQKMQOLEQMLTALDOMRBSIVSELAGLISAMEYVOKTITDEELADWKRRPEI 120
Db 190 GNNQSVTRQKMQOLEQMLTALDOMRBSIVSELAGLISAMEYVOKTITDEELADWKRRPEI 249
Qy 121 ACIGGPNNICLDRLNWTSLAESQIQTRQIQIKKLELOKQVSKYKGDPIVQHRPMLLEERI 180
Db 250 ACIGGPNNICLDRLNWTSLAESQIQTRQIQIKKLELOKQVSKYKGDPIVQHRPMLLEERI 309
Qy 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVTKTGQFATAVALLVKFPPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVTKTGQFTTKVRLLVKFPPEL 358

RESULT 9

US-08-956-652-12
; Sequence 12, Application US/08956652
; Patent No. 6013475
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,652
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-652-12

Query Match

98.8%; Score 1155; DB 3; Length 770;

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Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSQGDMDL 189
QY 61 GNNQSVTRQMKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSQGDMDL 120
Db 190 GNNQSVTRQMKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSQGDMDL 249
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Db 250 ACIGGPPNICLDRLENWITSLEASQLQTRQOIKKLELOQKVS YKGDPIVQHRPML 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 358

RESULT 10
US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12

Query Match 98.8%; Score 1155; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
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QY 61 GNNQSVTRQMKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSQGDMDL 120
Db 190 GNNQSVTRQMKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSQGDMDL 249
QY 121 ACIGGPPNICLDRLENWITSLEASQLQTRQOIKKLELOQKVS YKGDPIVQHRPML 180
Db 250 ACIGGPPNICLDRLENWITSLEASQLQTRQOIKKLELOQKVS YKGDPIVQHRPML 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 358

RESULT 11
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:

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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12

Query Match 98.8%; Score 1155; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 130 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDQDLN 189
QY 61 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRPEI 249
QY 121 ACIGGPNICLDRLNNWITS LAESQLTRQIQIKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPNICLDRLNNWITS LAESQLTRQIQIKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 358

RESULT 12
US-09-364-970-3
; Sequence 3, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-3

Query Match 98.8%; Score 1155; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 130 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDQDLN 189
QY 61 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRPEI 249
QY 121 ACIGGPNICLDRLNNWITS LAESQLTRQIQIKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPNICLDRLNNWITS LAESQLTRQIQIKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 358

US-09-364-970-3

RESULT 13
US-09-364-970-5
; Sequence 5, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-5

Query Match 98.8%; Score 1155; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 130 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDQDLN 189
QY 61 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRPEI 249
QY 121 ACIGGPNICLDRLNNWITS LAESQLTRQIQIKLEELQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPNICLDRLNNWITS LAESQLTRQIQIKLEELQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPPEL 358

RESULT 14
US-08-956-653A-12
; Sequence 12, Application US/08956653A
; Patent No. 6338949
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,653A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,185
; FILING DATE: 11-MAR-1994

;; APPLICATION NUMBER: US 07/980,498
;; FILING DATE: 23-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/854,296
;; FILING DATE: 19-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO US93/02569
;; FILING DATE: 19-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/126,588
;; FILING DATE: 24-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-195
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 770 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-956-653A-12

Query Match 98.8%; Score 1155; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDPFDNYKTLKSGQDMQDLN 60
Db 130 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDPFDNYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMOQLEOMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
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Db 250 ACIGGPPNICLDRLENWITSLSAQQLQTRQIQKLEELQKVSQKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 358

RESULT 15
US-08-212-185-12
; Sequence 12, Application US/08212185
; Patent No. 6605442
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/212,185
;; FILING DATE: 11-MAR-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/980,498
;; FILING DATE: 23-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/854,296
;; FILING DATE: 19-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO US93/02569
;; FILING DATE: 19-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/126,588
;; FILING DATE: 24-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 770 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-212-185-12

Query Match 98.8%; Score 1155; DB 4; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.6e-97;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDPFDNYKTLKSGQDMQDLN 60
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Db 250 ACIGGPPNICLDRLENWITSLSAQQLQTRQIQKLEELQKVSQKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKPEL 229
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1155	98.8	252	13	US-10-090-185-14
5	1155	98.8	271	13	US-10-090-185-9
6	1155	98.8	770	11	US-09-876-773-12
7	1155	98.8	770	17	US-10-639-617-12
8	1151	98.5	229	13	US-10-090-185-31
9	1150	98.4	229	13	US-10-090-185-30
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14	1144	97.9	770	14	US-10-038-010-56	Sequence 56, Appli
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19	1139	97.4	770	15	US-10-116-275-349	Sequence 19, Appl
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22	1027	87.9	223	13	US-10-090-185-22	Sequence 23, Appl
23	828	70.8	185	13	US-10-090-185-23	Sequence 16, Appl
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29	556	47.6	582	14	US-10-245-120-3	Sequence 6, Appli
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31	556	47.6	712	14	US-10-245-120-2	Sequence 6, Appli
32	556	47.6	712	17	US-10-639-617-6	Sequence 5, Appli
33	556	47.6	712	17	US-10-936-390-5	Sequence 2, Appli
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35	556	47.6	750	11	US-09-876-773-4	Sequence 4, Appli
36	556	47.6	750	14	US-10-245-120-1	Sequence 44, Appl
37	556	47.6	750	14	US-10-308-279-44	Sequence 352, App
38	556	47.6	750	16	US-10-755-889-352	Sequence 823, App
39	556	47.6	750	16	US-10-755-889-823	Sequence 19, Appl
40	556	47.6	750	17	US-10-492-043-19	Sequence 4, Appli
41	556	47.6	750	17	US-10-639-617-4	Sequence 550, App
42	556	47.6	786	9	US-09-925-297-550	Sequence 24, Appl
43	554	47.4	129	13	US-10-090-185-24	Sequence 6, Appli
44	549	47.0	749	9	US-09-833-205-6	Sequence 8, Appli
45	549	47.0	749	11	US-09-876-773-8	

ALIGNMENTS

RESULT 1

US-10-090-185-29
; Sequence 29, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-090-185-29

Query Match 100.0%; Score 1169; DB 13; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NHPTAAVTEKQMLQHLQVDRKRVODLEQKMKVVENLQDDFDNFYTKLSQSGMDLN 60
Db 1 NHPTAAVTEKQMLQHLQVDRKRVODLEQKMKVVENLQDDFDNFYTKLSQSGMDLN 60
Qy 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVOKLTLDLADWKRPEI 120
Db 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVOKLTLDLADWKRPEI 120


```
; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR P
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-090-185-9

Query Match          98.8%; Score 1155; DB 13; Length 271;
Best Local Similarity 98.7%; Pred. No. 3 9e-93;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDVKRKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 60
Db 24 NHPTAAVTEKQMLEQHLQDVKRKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 83
QY 61 GNNQSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
Db 84 GNNQSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 143
QY 121 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLEELQKYSYKGDPIVQHRPMLREI 180
Db 144 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLEELQKYSYKGDPIVQHRPMLREI 203
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 229
Db 204 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 252

RESULT 6
US-09-876-773-12
; Sequence 12, Application US/09876773
; Publication No. US20040058318A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,773
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match          98.8%; Score 1155; DB 11; Length 770;
Best Local Similarity 98.7%; Pred. No. 1 5e-92;
Matches 226; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDVKRKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVTEKQMLEQHLQDVKRKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
Db 190 GNNQSVTRQKMQOLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 249
QY 121 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLEELQKYSYKGDPIVQHRPMLREI 180
Db 250 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLEELQKYSYKGDPIVQHRPMLREI 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALIVKPEL 358

RESULT 7
US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-Aug-2003
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993

FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

ILEBA: 133921
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 770 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 12:
 10-639-617-12

Query Match	98.8%;	Score 1155;	DB 17;	Length 770;
Best Local Similarity	98.7%;	Pred. No. 1.5e-92;		
Matches 226;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	NHPTAAVVTEKQMLEOHLQDVRKRVQDLEQKMKVVENLQDDFNFYKTKLSQSGMDQDLN	60	
Db	130	NHPTAAVVTEKQMLEOHLQDVRKRVQDLEQKMKVVENLQDDFNFYKTKLSQSGMDQDLN	189	
Qy	61	GNNQSVTRQKMQOLEMLTALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI	120	
Db	190	GNNQSVTRQKMQOLEMLTALDQWRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI	249	
Qy	121	AC1GGPPNI CLDRLENNITSLAESQLOTRQOI KLEELQKQSVYKGGPI VQHRPMLSERI	180	
Db	250	AC1GGPPNI CLDRLENNITSLAESQLOTRQOI KLEELQKQSVYKGGPI VQHRPMLSERI	309	
Qy	181	VELFRNLKSAFVVERQPCPMHPDRPLVKTGTGQFATAVALLVKFPPEL	229	
Db	310	VELFRNLKSAFVVERQPCPMHPDRPLVKTGTGQFTTKVRLLLVKFPPEL	358	

RESULT 8
US-10-090-185-31
; Sequence 31, Application US/10090185
; Publication NO. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR E
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 31
; LENGTH: 229

```

; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-31

```

Query Match	98.5%	Score 1151;	DB 13;	Length 229;
Best Local Similarity	98.3%;	Pred. No. 7.1e-93;		
Matches 225; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	NHPTAAVVTKEQOMLEOHLQDVRRKRVQDLLEQKMKVVENLQDDDFNNYKTLKSQGDMDLNL	60	
Db	1	NHPTAAVVTKEQOMLEOHLQDARKRVQDLLEQKMKVVENLQDDDFNNYKTLKSQGDMDLNL	60	
Qy	61	GNNQSVTRQKMQOIEOMLTALDOMRRSIVSELAGLISAMEYVQKLTITDELDADWKRPEI	120	
Db	61	GNNQSVTRQKMQOIEOMLTALDOMRRSIVSELAGLISAMEYVQKLTITDELDADWKRPEI	120	
Qy	121	AC1GGPNICLDRLNWIITSLAESQLQTRQIIKKLELOQKVSYKGDPIVOHRPMLLEERI	180	
Db	121	AC1GGPNICLDRLNWIITSLAESQLQTRQIIKKLELOQKVSYKGDPIVOHRPMLLEERI	180	
Qy	181	VELFRNLMSAFVVERQPCNMPHDPRLVIKTGVGFATAVALIVKPPPEL	229	
Db	181	VELFRNLMSAFVVERQPCNMPHDPRLVIKTGVQFTTKVRLIVKPPPEL	229	

RESULT 9
US-10-090-185-30
? Sequence 30, Application US/10090185
? Publication No. US20020197647A1
? GENERAL INFORMATION:
? APPLICANT: Zhang, Xiaokui
? APPLICANT: Wrzeszczynska, Melissa H
? APPLICANT: Horvath, Curt M
? APPLICANT: Darnell Jr., James E
? TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
? TITLE OF INVENTION: INTERACTIONS
? FILE REFERENCE: 600-1-253
? CURRENT APPLICATION NUMBER: US/10/090,185
? CURRENT FILING DATE: 2002-03-04
? PRIOR APPLICATION NUMBER: 09/387,418
? PRIOR FILING DATE: 1999-08-31
? NUMBER OF SEQ ID NOS: 43
? SOFTWARE: PatentIn ver. 2.0
? SEQ ID NO 30
? LENGTH: 229
? TYPE: prt
? ORGANISM: Mus musculus
US-10-090-185-30

Query Match	98.4%;	Score 1150;	DB 13;	Length 229;
Best Local Similarity	98.3%;	Pred. No. 8.7e-93;		
Matches 225; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy 1	NHPTAAVTEKQOMLECHLQDVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDL	60		
Db 1	NHPTAAVTEKQOMLECHLQDVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDL	60		
Qy 61	GNQSVTRQKQOOLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDBELADWKRPEI	120		
Db 61	GNQSVTRQKQOOLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDBELADWKRPEI	120		
Qy 121	ACIGGPNPNCIDLENNWITSIAESQLOTRQOIKKLEELQOKYSYKGDPIVQHRPMLERI	180		
Db 121	ACIGGPNPNCIDLENNWITSIAESQLOTRQOIKKLEELQOKYSYKGDPIVQHRPMLERI	180		
Qy 181	VELFRNLMSAFVVERQPCMPMPDRPLVIKTVGVQFATAVALLVPPEL	229		
Db 181	VELFRNLMSAFVVERQPCMPMPDRPLVIKTVGVQFATAVALLVPPEL	229		

RESULT 10
US-10-380-020-4
; Sequence 4, Application US/10380020

Publication No. US20040052762A1
GENERAL INFORMATION:
APPLICANT: Yu, Hua
APPLICANT: Fardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Dalton, William
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 720
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-380-020-4

Query Match 97.9%; Score 1144; DB 15; Length 720;
Best Local Similarity 97.8%; Pred. No. 1.1e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 120
DB 190 GNNQSVTRQKMQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 249
QY 121 ACIGPPNCLDRLENWITSLAESQLQTRQIQKLEELQKMKVVENLQDDDFNYKTLKSGQDMQDLN 180
DB 250 ACIGPPNCLDRLENWITSLAESQLQTRQIQKLEELQKMKVVENLQDDDFNYKTLKSGQDMQDLN 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 358

RESULT 11
US-10-380-020-2
Sequence 2, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
APPLICANT: Yu, Hua
APPLICANT: Fardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Dalton, William
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 769
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match 97.9%; Score 1144; DB 15; Length 769;
Best Local Similarity 97.8%; Pred. No. 1.1e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 120

DB 190 GNNQSVTRQKMQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189
QY 121 ACIGPPNCLDRLENWITSLAESQLQTRQIQKLEELQKMKVVENLQDDDFNYKTLKSGQDMQDLN 180
DB 250 ACIGPPNCLDRLENWITSLAESQLQTRQIQKLEELQKMKVVENLQDDDFNYKTLKSGQDMQDLN 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 358

RESULT 12
US-10-380-020-5
Sequence 5, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
APPLICANT: Yu, Hua
APPLICANT: Fardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Dalton, William
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 769
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-380-020-5

Query Match 97.9%; Score 1144; DB 15; Length 769;
Best Local Similarity 97.8%; Pred. No. 1.1e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 120
DB 190 GNNQSVTRQKMQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 249
QY 121 ACIGPPNCLDRLENWITSLAESQLQTRQIQKLEELQKMKVVENLQDDDFNYKTLKSGQDMQDLN 180
DB 250 ACIGPPNCLDRLENWITSLAESQLQTRQIQKLEELQKMKVVENLQDDDFNYKTLKSGQDMQDLN 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKPEL 358

RESULT 13
US-10-045-792-8
Sequence 8, Application US/10045792
Publication No. US20030003563A1
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
Moarefi, Ismail
Darnell, Jr., James E.
Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
CORRESPONDENCE ADDRESS: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey

;
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,792
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8

Query Match 97.9%; Score 1144; DB 14; Length 770;
Best Local Similarity 97.8%; Pred. No. 1.4e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWKRRQOI 249
QY 121 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVKSYKGDPIVQHRPMLERI 180
DB 250 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVKSYKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFATAVALLVKPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFATAVALLVKPPEL 358

RESULT 14
US-10-038-010-56
; Sequence 56, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens

;
; FEATURE:
; NAME/KEY: STAT3 : Transcription factor
; LOCATION: (1)..(770)
; OTHER INFORMATION:
US-10-038-010-56
Query Match 97.9%; Score 1144; DB 14; Length 770;
Best Local Similarity 97.8%; Pred. No. 1.4e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWKRRQOI 249
QY 121 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVKSYKGDPIVQHRPMLERI 180
DB 250 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVKSYKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFATAVALLVKPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFATAVALLVKPPEL 358

RESULT 15
US-10-117-087-2
; Sequence 2, Application US/10117087
; Publication No. US20030166854A1
; GENERAL INFORMATION:
; APPLICANT: SERLUP1-CRESCENZI, Ottaviano
; APPLICANT: DELLA PIETRA, Linda
; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
; FILE REFERENCE: SERLUP1-2
; CURRENT APPLICATION NUMBER: US/10/117,087
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/526,542
; PRIOR FILING DATE: 2000-03-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Human
US-10-117-087-2

Query Match 97.9%; Score 1144; DB 14; Length 770;
Best Local Similarity 97.8%; Pred. No. 1.4e-91;
Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWKRRQOI 249
QY 121 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVKSYKGDPIVQHRPMLERI 180
DB 250 ACIGGPPNICLDRLNNWITSLSAESQLQTRQOIKKLEELQKVKSYKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFATAVALLVKPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFATAVALLVKPPEL 358

Search completed: May 25, 2005, 18:21:53
Job time : 101.62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:24:07 ; Search time 21.6038 Seconds
(without alignments)
1019.898 Million cell updates/sec

Title: US-10-090-185-29
Perfect score: 1169
Sequence: 1 NHPTAAVTEKQOMLEQHLQ.....IKTGQFATAVALLVKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1144	97.9	770	2 I49508	ISGF3 p91-related
2	1139	97.4	770	2 A54444	DNA-binding protei
3	510.5	43.7	739	2 A46159	interferon-depende
4	495	42.3	748	2 A56047	gamma-interferon a
5	310	26.5	851	2 A46160	interferon alpha-1
6	269.5	23.1	786	2 I49274	mammary gland fact
7	269.5	23.1	793	2 S54772	mammary gland fact
8	263.5	22.5	794	2 G02317	transcription acti
9	238	20.4	794	2 S55527	mammary gland fact
10	126	10.8	978	2 A70387	conserved hypothet
11	124	10.6	533	2 G72593	hypothetical prote
12	122	10.4	848	2 A54742	interleukin-4-indu
13	120.5	10.3	837	2 I57557	DNA-Binding Protei
14	119.5	10.2	1166	2 T27075	hypothetical prote
15	118.5	10.1	1208	2 AE1947	chromosome segrega
16	118.5	10.1	2094	2 S33124	tpv protein - huma
17	115.5	9.9	924	2 S06117	myosin heavy chain
18	115	9.8	1164	2 T24806	hypothetical prote
19	114.5	9.8	2007	1 B43402	myosin heavy chain
20	114	9.8	1976	2 A59252	myosin heavy chain
21	113.5	9.7	727	2 AC1814	hypothetical prote
22	113.5	9.7	857	2 S33821	median body protei
23	112.5	9.6	946	2 S28061	SCP1 protein - rat
24	112.5	9.6	1690	2 T13030	microtubule bindin
25	112.5	9.6	1957	2 T38077	hypothetical coile
26	112.5	9.6	2253	2 T30336	nuclear/mitotic ap
27	112	9.6	289	2 S51193	epimorphin - mouse
28	112	9.6	1509	1 A27224	myosin heavy chain
29	112	9.6	1999	1 S21801	myosin heavy chain

30	111.5	9.5	284	2 C64527	M protein - Helico
31	111.5	9.5	1048	1 BVECS	exonuclease (EC 3.
32	111	9.5	1959	1 A33977	myosin heavy chain
33	110.5	9.5	747	1 A57107	kinesin-related pr
34	110.5	9.5	1940	1 A59287	myosin heavy chain
35	110.5	9.5	1992	2 A47297	myosin heavy chain
36	110	9.4	1188	2 G83960	chromosome segrega
37	110	9.4	2020	2 T21174	hypothetical prote
38	109.5	9.4	434	2 T43448	hypothetical prote
39	109.5	9.4	527	2 S33068	myosin heavy chain
40	109.5	9.4	734	2 T27055	hypothetical prote
41	109.5	9.4	896	2 S43074	epidermal growth f
42	109.5	9.4	1047	2 C85535	ATP-dependent dsDN
43	109.5	9.4	1047	2 G90684	ATP-dependent dsDN
44	109.5	9.4	1738	2 T14867	interaptin - slime
45	109.5	9.4	3685	1 A27605	dystrophin, muscle

ALIGNMENTS

RESULT 1

I49508

ISGF3 p91-related transcription factor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49508; I49009

R:Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su

Cell 77, 63-71, 1994

A>Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr

A:Reference number: A54444; MUID:94208062; PMID:7512451

A:Accession: I49508

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-770 <RES>

A:Cross-references: UNIPROT:P42227; GB:I29278; NID:G476715; PIDN:AAA37254.1; PID:G47671

R:Baz, R.; Durbin, J.E.; Levy, D.E.

J. Biol. Chem. 269, 24391-24395, 1994

A>Title: Acute phase response factor and additional members of the interferon-stimulate

A:Reference number: I49009; MUID:95014185; PMID:7523373

A:Accession: I49009

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-393, 'M', 395-700, 702-770 <RE2>

A:Cross-references: EMBL:U08378; NID:G473889; PIDN:AAA56668.1; PID:G473890

C:Genetics:

A:Gene: APRF

C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 97.9%; Score 1144; DB 2; Length 770;

Best Local Similarity 97.8%; Pred. No. 1e-68;

Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY	1	NHPTAAVTEKQOMLEQHLQDVVRKVQDLEQKMKVVENLQDDPFNFYKTLKSGQDMQDLN	60
DB	130	NHPTAAVTEKQOMLEQHLQDVVRKVQDLEQKMKVVENLQDDPFNFYKTLKSGQDMQDLN	189
QY	61	GNNQSVTRQKMOOLEQMLTALDOMERSIVSELAGLLSAMEYVQKTLTDELDWKRPET	120
DB	190	GNNQSVTRQKMOOLEQMLTALDOMERSIVSELAGLLSAMEYVQKTLTDELDWKRPET	249
QY	121	ACIGGPPNICLDLENWITSLSAESOLQTRQQLKLEELQKQVSKGDPVQHRPMLERI	180
DB	250	ACIGGPPNICLDLENWITSLSAESOLQTRQQLKLEELQKQVSKGDPVQHRPMLERI	309
QY	181	VELFRNLKMSAFVVRQPCMPHDPRLVKTGVQFATAVALLVKPPEL	229
DB	310	VELFRNLKMSAFVVRQPCMPHDPRLVKTGVQFATAVALLVKPPEL	358

RESULT 2

A54444

DNA-binding protein APRF - human

A;Reference number: S53873; MUID:95192056; PMID:7885841

A;Accession: S53873

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-196;392-591;684-730 <YAW>

A;Cross-references: EMBL:U18671

C;Genetics:

A;Gene: stat2

A;Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; 40

C;Superfamily: human signal transducer and transcription activator STAT5A

C;Keywords: signal transduction; transcription regulation

Query Match 26.5%; Score 310; DB 2; Length 851;

Best Local Similarity 32.8%; Pred. No. 3.7e-13;

Matches 72; Conservative 51; Mismatches 92; Indels 6; Gaps 4;

QY 8 VTEKQQLQHLQDVRKRVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNGNQSVT 67

DB 138 VESQHEIESRIILDLAMWEKLVKISQLXQDDVCFRYK-IOAKGKTPSLDPH--QTK 194

QY 68 RQMQQLQMLTALDQWRRSIVSELAGLSAMEYVQKTLTDEELADWRKRPEIACIGGPP 127

DB 195 EQKI--LQETNELDKRRKEVLDASKALLGRLLFTLIELLL-PKLEWKAQQQKACIRAPI 251

QY 128 NCLDLLENWITSLSAQSLQTRQIKLEELQKQVSGDPVQHRPMLERIVELFRML 187

DB 252 DHGLEQLFTWFTAGAKLLFHLRLKELGSLVSYQDDPLTKGVDLRNAQVTELLQRL 311

QY 188 MKSAFVVERQPCMPHDPRLVKTGVQFATAVALLVKKPE 228

DB 312 LHRAFVETQPCMPQTPHRPLILKTGSKFTVTRLLVRLQE 352

RESULT 6

I49274

mammary gland factor - mouse

N;Alternate names: STAT5 protein homolog p80

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49274; S54773; S54727

R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved in

A;Reference number: I49273; MUID:96004632; PMID:7568026

A;Accession: I49274

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-786 <RES>

A;Cross-references: UNIPROT:P42232; UNIPROT:Q9UKM1; EMBL:U21110; NID:g747973; PIDN:AA052

R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A;Reference number: S54772; MUID:95237198; PMID:7720707

A;Accession: S54773

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-432,'E',434-786 <MUI>

A;Cross-references: EMBL:248539; NID:g758635; PIDN:CAA8420.1; PID:g758636

R;Azam, M.; Erdjument-Bronage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,

EMBO J. 14, 1402-1411, 1995

A;Title: Interleukin-3 signals through multiple isoforms of Stat5.

A;Reference number: S54725; MUID:95246733; PMID:7537213

A;Accession: S54727

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-432,'E',434-786 <AZA>

C;Genetics:

A;Gene: Stat5b

C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match

Best Local Similarity 23.1%; Score 269.5; DB 2; Length 786;

Matches 71; Conservative 42; Mismatches 98; Indels 21; Gaps 5;

transcription activator stat5a - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

QY 5 AAVVTEKQQLQHLQDVRKRVDLEQKMKVVENLQDDFDNFY-KTLKSGQDMQDLNGNN 63

DB 134 ADAMSQKHLQINQTFEELRLITQDTENELKCLQOTQYFIQYQESLRIOAQFAQLGQLN 193

QY 64 -----QSVTRQKMQQLQEQML-----TALDQMRRSIVSELAGLSAMEYVQKTLTDEELA 112

DB 194 POERMSRETALQKQVSLQVETWLOREAQTLQYRVLAELAEKHQKTLQLLRKQQTILDDLELI 253

QY 113 DWKRRPEIACIGPPNCLDRLENWITSLSAQSLQTRQIKLEELQKQVSGDPVQHRPMLERIVELFRML 172

DB 254 QWKRQQLAGNGPPGSLDVLSQWCEKLAETIWNQRIIRRAEHLCCQQLPIFG-PVEEM 312

QY 173 RPLMERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLV 224

DB 313 LAEVNATITDIISALVTSTFIIEKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 7

S54772

mammary gland factor - mouse

N;Alternate names: stat5 protein

C;Species: Mus musculus (house mouse)

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S54772; I49273

R;Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A;Reference number: S54772; MUID:95237198; PMID:7720707

A;Accession: S54772

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-793 <MUI>

A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:Z48538; NID:g758633; PIDN:CAA8

R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved

A;Reference number: I49273; MUID:96004632; PMID:7568026

A;Accession: I49273

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-793 <RES>

A;Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972

C;Genetics:

A;Gene: Stat5a

C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match

Best Local Similarity 23.1%; Score 269.5; DB 2; Length 793;

Matches 70; Conservative 42; Mismatches 96; Indels 21; Gaps 5;

QY 8 VTEKQQLQHLQDVRKRVDLEQKMKVVENLQDDFDNFY-KTLKSGQDMQDLNGNN--- 63

DB 137 MSQKHLQINQRFEEELRLITQDTENELKCLQOTQYFIQYQESLRIOAQFAQLGQLNPQE 196

QY 64 -----QSVTRQKMQQLQEQML-----TALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWK 115

DB 197 RMSRETALQKQVSLQVETWLOREAQTLQYRVLAELAEKHQKTLQLLRKQQTILDDLELIQWK 256

QY 116 RPETIACIGPPNCLDRLENWITSLSAQSLQTRQIKLEELQKQVSGDPVQHRPMLERIVELFRML 175

DB 257 RQQLAGNGPPGSLDVLSQWCEKLAETIWNQRIIRRAEHLCCQQLPIFG-PVEEMLAELAE 315

QY 176 LEERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLV 224

DB 316 VNATITDIISALVTSTFIIEKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 8

G02317

transcription activator stat5a - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C;Accession: G02317
R;Lin, J.
Submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:g1151169; PIDN:AAB06589.1; PID:g1151169
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.5%; Score 263.5; DB 2; Length 794;
Best Local Similarity 30.1%; Pred. No. 4.3e-10;
Matches 69; Conservative 43; Mismatches 96; Indels 21; Gaps 5;

QY 8 VTEKQMLEQHLQDVRKRVQDLEQKMKVENLQDDFDNFY-KTLKSGDQMDL----- 59
DB 137 MSQKHQINQTFEELRLVTDTENELKQLOQTQYFIQYQESLRIOAQFAQLSPQE 136
QY 60 NGNNQSVTRQKMOLEQML-----TALDQRRSIVSELAGLLSMEYVQKTLTDEELADWK 115
DB 197 RLSRETALQKQVSLQVLEAWLQREAGTQLOQYRVLAERKHQTLQLLRKQQTILDELQIWK 256
QY 116 RRPFIACIGPPNCLDRLENWITSLSAESQLQTRQIKKLEELQKQVSKGDPVQHRPM 175
DB 257 RRQOLAGNGPPGSLDVLQSWCKELAEIITWQNRQRIIRAEHLCCQLPIFG-PVEEMLAE 315
QY 176 LEERIVELFRLNLMKSAFVVERQPCMPHDPRLVKTGVQFATAVALLV 224
DB 316 VNATITDIISALVTSTFIIIEKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 9
S55527
mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55527; S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regulat
A;Reference number: S55527; MUID:9518889; PMID:7882987
A;Accession: S55527
A;Molecule type: mRNA
A;Residues: 1-794 <WAK>
A;Cross-references: UNIPROT:P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g6023
A;Note: This is a revision to the sequence from reference S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 13, 2182-2191, 1994
A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcri
A;Reference number: S44353; MUID:94244619; PMID:7514531
A;Accession: S44353
A;Molecule type: mRNA
A;Residues: 1-716, 'RHLHGSLPSR', 729, 'P', 731, 'ASL', 'WAW'
A;Cross-references: EMBL:X78428
A;Note: This sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 20.4%; Score 238; DB 2; Length 794;
Best Local Similarity 29.3%; Pred. No. 2.1e-08;
Matches 67; Conservative 42; Mismatches 98; Indels 22; Gaps 6;

QY 8 VTEKQMLEQHLQDVRKRVQDLEQKMKVENLQDDFDNFY-KTLKSGDQMDLNGN--- 63
DB 138 MSQKHQINQTFEELRLVTDTENELKQLOQTQYFIQYQESLRIOAQFAQLNPQE 197
QY 64 ----QSVTRQKMOLEQML-----TALDQRRSIVSELAGLLSMEYVQKTLTDEELADWK 115
DB 198 RLSRETALQKQVSLQVLEAWLQREAGTQLOQYRVLAERKHQTLQLLRKQQTILDELQIWK 257
QY 116 RRPFIACIGPPNCLDRLENWITSLSAESQLQTRQIKKLEELQKQVSKGDPVQHRPM 175
DB 258 RRHDWRGMEAPPR-SLDVLQSWCKELAEIITWQNRQRIIRAEHLCCQLPIFG-PVEEMLAE 315

QY 176 LEERIVELFRLNLMKSAFVVERQPCMPHDPRLVKTGVQFATAVALLV 224
DB 316 VNATITDIISALVTSTFIIIEKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 10
A70387
conserved hypothetical protein aq_1006 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A70387
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O.
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: A70387
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-978 <AQF>
A;Cross-references: UNIPROT:O67124; GB:AE000718; NID:g2983504; PIDN:AAC07092.1; PID:g29;
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_1006
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match 10.8%; Score 126; DB 2; Length 978;
Best Local Similarity 23.8%; Pred. No. 0.77;
Matches 50; Conservative 38; Mismatches 80; Indels 42; Gaps 6;

QY 10 EKQOMLEQHLQDVRKRVQDLEQKMKVENLQDDFDNFYKTLKSGDQMDLNGNNSVTRQ 69
DB 234 EKQSLERLSQVTVTKLELENLEKEVEKLEKLEFSRVAP-----YVPIAK 281
QY 70 KMQQLQMLTALDQRRSIVSELAGLLSMEYVQKTLT-----DEELAD- 113
DB 282 RIEIDKKLTTELKVRKNKLTKEALVLDKELSPAQELNRIEAEKFEKEKEKELEHR 341
QY 114 WKRPFIACIGPPNCLDRLENWITSLSAESQLQTRQIKKLEELQKQVSKGDPVQHR 173
DB 342 LKKLQBIKEI-----LKELSQLSSLSKEKEVEYQAKQEFEDLSERVE-KGKKLVAET 393
QY 174 PMLERIVELERN-----LMKSAFVVERQ 197
DB 394 EKLEKIKELFSEETSLMKMERLIVELQ 423

RESULT 11
G72593
hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72593
R;Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72593
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-533 <KAW>
A;Cross-references: UNIPROT:Q9YCP2; DDBJ:AF000061; NID:g5104821; PIDN:BAH80205.1; PID:;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1216

Query Match 10.6%; Score 124; DB 2; Length 533;
Best Local Similarity 21.2%; Pred. No. 0.52;
Matches 42; Conservative 49; Mismatches 65; Indels 42; Gaps 7;

QY 8 VTEKQMLEQHLQDVRKRVQDLEQKMKVVEN-----LQDDF-----DFNYK 48

Db 319 MSQQLALAEEDLESRSVEDLEARVGSVEDRLSQAEDDIDSLTTSLSRLTELEDLSR 378
QY 49 TLKSGQDMQDLNGNNSVTRQKMQQLQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLD 108
Db 379 LAEAQASLEDLNLRLDQVA-STLQQLQORLATAEESLQALTEDLASLQAEVETLQQSIVE 437
QY 109 BELADWKRRPPIACIGPPNICLDRLNWTSLAESQLQ-----TROQIKLLELQKVSY 164
Db 438 IDRLQLRLSTDAV-----RLE--VESLGEKLVAQAEKNQRQDASIEDFQSIQ- 485
QY 165 KGDPIVQHRPMLERIVE 182
Db 486 -----ELRTQDEKTR 497

RESULT 12

A54740
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: A54740
R:Hou, J.; Schindler, U.; Hensel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
Science 265, 1701-1706, 1994
A:Title: An interleukin-4-induced transcription factor: IL-4 stat.
A:Reference number: A54740; MUID:94367369; PMID:8085155
A:Accession: A54740
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-848 <HOU>
A:Cross-references: UNIPROT:P42226
C:Superfamily: human signal transducer and transcription activator STAT5A
C:Keywords: DNA binding; transcription regulation

Query Match 10.4%; Score 122; DB 2; Length 848;
Best Local Similarity 24.3%; Pred. No. 1.2; Indels 50; Gaps 9;
Matches 58; Conservative 37; Mismatches 94

QY 3 PTAAVVTEKQMLEHLQDVRKRVQDLEQKMKVVENLQDDDFNFYTKLSQSGMDQNLGN 62
Db 92 PLKLVA-----PRLQLOKKAV-----MEQFRLPWPFWKQBELKFKTGLRLQHR 140
QY 63 NOSV--TRQKMQ-----LEQML-----TALDQMRRSIVSELAGLLSAMEYVQKYL 106
Db 141 VGEIHLRLALQGAAGQVSLHSLETPTANGTGPSEALMLQIQTTSLEA-----AKAL 196
QY 107 TDELDWKRRPPIACIGPPNICLDRLNWTSLAESQLQOTQOIKLEELQKVSYKG 166
Db 197 VLKRIQIWRKQQLANGAP-----FEESLAPQERCSLVDIYSQLOQVGAAG 246
QY 167 DPI-VQHRPMLERIVELEFNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLV 224
Db 247 GELEPKTRASLTGLDEVLTIVTSFLVEKQP-----PQVLKTKYKFGQVRFLL 297

RESULT 13

I57557
DNA-Binding Protein and transcription factor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I57557
R:Quelle, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Cleve
Mol. Cell. Biol. 15, 3336-3343, 1995
A:Title: Cloning of murine Stat6 and human Stat6, Stat proteins that are tyrosine phosph
A:Reference number: I57557; MUID:95280934; PMID:7760829
A:Accession: I57557
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-837 <RES>
A:Cross-references: UNIPROT:P52633; GB:I47650; NID:g1008876; PID:AAA79006.1; PID:g10088
C:Genetics:
A:Gene: STAT6
C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 10.3%; Score 120.5; DB 2; Length 837;
Best Local Similarity 25.8%; Pred. No. 1.5; Indels 59; Gaps 10;
Matches 60; Conservative 31; Mismatches 83

QY 10 EKQOMLEQ--HLQDVRKRVQD-----LEQKMKVVENLQDDDFNFYTKLSQSGDMQ 57
Db 106 EKAVIEEPFHLPGFPHRKQBELKFTTPLGRLLHVRVRETRLLRESLHGPKT--GQVSLQ 163
QY 58 D-----LNGNNSVTRQKMQQLQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELA 112
Db 164 NLIDPPLNGPGFS-----EDLPTILQ-----GTVGDLTTQ-PLVLLRIQ 202
QY 113 DWKRRPPIACIGPPNICLDRLNWTSLAESQLQOTQOIKLE-ELQKVKSYKGDPIVQ 171
Db 203 IWKROOQLAGNCTPFESLAGQERCSLVEIYSQHLQHGAASGELEPKT----- 253
QY 172 HRPMLERIVELEFNLKMSAFVVERQPCMPHDPRLVKTGVQFATAVALLV 224
Db 254 -RASLISRLDEVLRTLVTSFLVEKQP-----PQVLKTKYKFGQVRFLL 297

RESULT 14

T27075
hypothetical protein Y51A2D.16 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27075
R:McMurray, A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20307
A:Accession: T27075
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1166 <WIL>
A:Cross-references: EMBL:AL021497; PIDN:CAA16403.1; GSPDB:GN00023; CESP:Y51A2D.16
A:Experimental source: clone Y51A2D
C:Genetics:
A:Gene: CESP:Y51A2D.16
A:Map position: 5
A:Introns: 17/3; 45/1; 76/2; 156/3; 240/2; 288/2; 594/2; 657/3; 756/3; 798/2; 900/3; 94

Query Match 10.2%; Score 119.5; DB 2; Length 1166;
Best Local Similarity 21.4%; Pred. No. 2.6; Indels 73; Gaps 9;
Matches 52; Conservative 46; Mismatches 72

QY 1 NHPTAAVTEKQ---QMLEQHLQD-----VRKRVQDLEQKMKVVENLQDD 42
Db 430 SHVTRLSLSEKTKLAKLE--LQDQVEAQTLLELNQKNGKRLERDQMI SNHLKNE 487
QY 43 FDFNYTKLSQSGMDQDLNGNNSVTRQKMQQLQMLTALDQMRRSIVSELAGLLSAMEY- 101
Db 488 LENDLTKCTQOLELES-----KKLQRLREDLVLEKSRREADLIGRIHSICTTSLN 537
QY 102 ---VQKLTDEELAD-----WTKRREIACIGPPNI----- 129
Db 538 GANFEKINDDDELIDNIDIMNALVAVKRRERDRLIQGNQOIQELHDLKRDIEKLRSR 597
QY 130 --CLDLENWITSLEASQLQTRQOI---KLEELQKVKSYKGDPIVQHRPMLERIVE 183
Db 598 SSLSNESDRVRELTRENHMTKEQVFMLOKRELNLSTKNDEI-----DMVKASIEEL 653
QY 184 FRN 186
Db 654 NRN 656

RESULT 15

AE1947
chromosome segregation protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C/Superfamily: chromosome segregation protein SMC1

153 -----KKLEELQQKV-SYKGDPIVQHRPMLLEERIVELFRNLKMSAF 192

Search completed: May 25, 2005, 17:45:28
Job time : 22.6038 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:15:30 ; Search time 95.284 Seconds
(without alignments)

1230.701 Million cell updates/sec

Title: US-10-090-185-29

Perfect score: 1169

Sequence: 1 NHPTAAVTEKQMLQHLQ.....IKTGVPQATAVALLVRFPEL 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1144	97.9	770	1 STA3 HUMAN	P40763 homo sapien
2	1144	97.9	770	1 STA3 MOUSE	P42227 mus musculus
3	1141	97.6	770	1 STA3 RAT	P52631 rattus norv
4	1137	97.3	770	1 STA3 BOVIN	P61635 bos taurus
5	1119	95.7	771	2 Q6DV79	O6dv79 gallus gall
6	1086	92.9	769	2 Q9PVX8	Q9pvx8 xenopus lae
7	1083	92.6	766	2 Q7ZXX3	Q7ztx3 brachydanio
8	998	85.4	414	2 Q7ZTS5	Q7zts5 oryzias lat
9	998	85.4	765	2 Q6DVF3	O6dvf3 oryzias lat
10	998	85.4	785	2 Q6GUE7	O6gue7 oryzias lat
11	998	85.4	786	2 Q6NV46	Q6nv46 brachydanio
12	998	85.4	806	2 Q93599	Q93599 brachydanio
13	974	83.3	764	2 Q90Y16	Q90y16 tetraodon f
14	964	82.5	767	2 Q13133	O13133 oncorhynch
15	639	54.7	163	2 Q9N145	Q9n145 macaca mula
16	562	48.1	751	2 Q8JGN0	O8jgn0 xenopus lae
17	560	47.9	712	2 Q6PGQ7	Q6pgq7 rattus norv
18	560	47.9	749	2 Q9QXK0	Q9qxx0 rattus norv
19	558	47.7	749	2 Q8CA97	Q8ca97 mus musculus
20	557	47.6	712	2 Q99K94	Q99k94 mus musculus
21	557	47.6	749	2 Q8C3V4	Q8c3v4 mus musculus
22	557	47.6	749	2 Q8D323	Q8d323 mus musculus
23	557	47.6	755	2 Q8C8M3	Q8cm83 mus musculus
24	556	47.6	750	1 STA1 HUMAN	P42224 homo sapien
25	556	47.6	750	2 Q68D00	Q68d00 homo sapien
26	556	47.6	757	2 Q764M5	Q764m5 sus scrofa
27	549	47.0	749	1 STA1 MOUSE	P42225 mus musculus
28	532.5	45.6	108	2 Q704W6	Q704w6 bos taurus
29	525.5	45.0	754	2 Q13131	O13131 oncorhynch
30	519	44.4	749	2 Q93598	Q93598 brachydanio
31	519	44.4	749	2 Q6P943	Q6p943 brachydanio

RESULT 1

ID	STA3 HUMAN	STANDARD;	PRT;	770 AA.
AC	P40763; O14916; Q9BW54;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Signal transducer and activator of transcription 3 (Acute-phase response factor).			
GN	Name=STAT3; Synonyms=APRF;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Placenta;			
RX	MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;			
RA	'Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T., Yoshida K., Sudo T., Naruto M., Kishimoto T.;			
RT	"Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling pathway.";			
RT	Cell 77:63-71(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;			
RA	Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;			
RT	"Highly conserved amino-acid sequence between murine STAT3 and a revised human STAT3 sequence.";			
RL	Gene 213:119-124(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.			
RA	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O., Rajkumar N., Yi Q., Nickerson D.A.;			
RT	"SeattlesNP. NHLBI HL66682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RT	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).			
RC	TISSUE=Kidney, and Pancreas;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			

Q8jfu8 brachydanio
Q80ly2 carassius a
Q14765 homo sapien
Q90y17 tetraodon f
O13132 oncorhynch
Q8aw24 brachydanio
P42228 mus musculus
Q7z253 brachydanio
Q8aw20 brachydanio
Q7z277 brachydanio
Q8jfu7 brachydanio
O66hb2 rattus norv
Q8jfs5 brachydanio
Q90y15 tetraodon f

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttsfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 564-704 FROM N.A.
 RC TISSUE=Liver;
 RA Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP PHOSPHORYLATION ON SERINE
 RX MEDLINE=95215843; PubMed=7701321;
 RA Zhang X., Bienis J., Li H.-C., Schindler C., Chen-Kiang S.;
 RT "Requirement of serine phosphorylation for formation of STAT-promoter
 RT complexes.";
 RL Science 267:1990-1994(1995).
 RN [7]
 RP INTERACTION WITH NCOAL
 RX PubMed=11773079; DOI=10.1074/jbc.M111486200;
 RA Graud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.;
 RT "Functional interaction of STAT3 transcription factor with the
 RT coactivator NcoA/SRC1a.";
 RL J. Biol. Chem. 277:8004-8011(2002).
 CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes.
 CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Names=1;
 CC IsoId=P40763-1; Sequence=Displayed;
 CC Names=Del-701;
 CC IsoId=P40763-2; Sequence=VSP_010474;
 CC -1- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
 CC muscle, kidney and pancreas.
 CC -1- PM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity.
 CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -----
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 CC EMBL; AJ012463; CAA10032.1; -;
 CC EMBL; AY572796; AAS66986.1; -;
 CC EMBL; BC000627; AAH00627.1; -;
 CC EMBL; BC014482; AAH14482.1; -;
 CC EMBL; AF029311; AAB84254.1; -;
 CC PIR; A54444; A54444.
 CC HSSP; P42227; 1BG1.
 CC TRANSFAC; T01493; -;
 CC Genew; HGNC:11364; STAT3.
 CC H-TnvdB; HIX0013840; -;
 CC MIM; 102582; -;
 CC GO; GO:0005737; C:cytoplasm; TAS.
 CC GO; GO:0005634; C:nucleus; TAS.
 CC GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. . .; TAS.

DR GO; GO:0003700; F:transcription factor activity; TAS.
 DR GO; GO:0006928; P:cell motility; TAS.
 DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
 DR GO; GO:0000122; P:negative regulation of transcription from P. . .; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF001017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 KW PROSITE; PS50001; SH2; 1.
 KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
 KW Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
 KW DOMAIN 580 670
 FT MOD_RES 705 705 Phosphotyrosine (by JAK) (by similarity).
 FT MOD_RES 727 727 Phosphoserine (by similarity).
 FT VARSPLIC 701 701 Missing (in isoform Del-701).
 FT VARIANT 32 32 Q -> K (in dbSNP:1803125).
 FT VARIANT 143 143 M -> I.
 FT CONFLICT 288 288 /FTID=VAR_018679.
 FT CONFLICT 460 460 Q -> H (in Ref. 1).
 FT CONFLICT 548 548 P -> S (in Ref. 1).
 FT CONFLICT 561 561 K -> N (in Ref. 1).
 FT CONFLICT 561 561 F -> Y (in Ref. 1).
 FT CONFLICT 667 667 V -> L (in Ref. 1).
 FT CONFLICT 730 730 T -> A (in Ref. 1).
 SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
 Query Match 97.9%; Score 1144; DB 1; Length 770;
 Best Local Similarity 97.8%; Pred. No. 4.3e-62;
 Matches 224; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLQEKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 DB 130 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLQEKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQMQOQLQOMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 120
 DB 190 GNNQSVTRQMQOQLQOMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRRQOI 249
 QY 121 ACIGGPNICLDLENWITSLAESQIQTRQIQIKLELOKQVSKGDPVQHRPMLLEERI 180
 DB 250 ACIGGPNICLDLENWITSLAESQIQTRQIQIKLELOKQVSKGDPVQHRPMLLEERI 309
 QY 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPEL 229
 DB 310 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFATAVALLVKFPEL 358
 RESULT 2
 STAJ MOUSE
 ID STAJ3 MOUSE STANDARD; PRT; 770 AA.
 AC P42227;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3 (Acute-phase
 DE response factor).
 GN Name-Stat3; Synonyms=Aprf;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
 RP AND 632-640.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;

RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
 RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
 RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
 RT related transcription factor involved in the gp130-mediated signaling
 RT pathway.";
 RL Cell 77:63-71(1994).
 RN [2]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC
 RX TISSUE=Thymus;
 RX MEDLINE=94188718; PubMed=8140422;
 RA Zhong Z., Wen Z., Darnell J.E. Jr.;
 RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
 RT response to epidermal growth factor and interleukin-6.";
 RL Science 264:95-98(1994).
 RN [3]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC
 RX TISSUE=Brain;
 RX MEDLINE=95014185; PubMed=7523373;
 RA Raz R., Durbin J.E., Levy D.E.;
 RT "Acute phase response factor and additional members of the interferon-
 RT stimulated gene factor 3 family integrate diverse signals from
 RT cytokines, interferons, and growth factors.";
 RL J. Biol. Chem. 269:24391-24395(1994).
 RN [4]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM STAT3B).
 RC STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
 RX MEDLINE=96016116; PubMed=7568080;
 RA Schaefer T.S., Sanders L.K., Nathans D.;
 RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
 RT form of Stat3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
 RN [5]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC STRAIN=129/SVJ;
 RX PubMed=11161808; DOI=10.1006/geno.2000.6433;
 RA Miyoshi K., Qui Y., Riedinger G., Lehoczy J., Zon L., Oka T.,
 RA Dewar K., Hennighausen L.;
 RT "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
 RT zebrafish to mouse.";
 RL Genomics 71:150-155(2001).
 RN [6]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC STRAIN=C57BL/6J, and NOD/LtJ;
 RA Davoodi-Semirani A., She J.-X.;
 RT "A mutant Stat5b with weaker DNA binding defines a key defective
 RT pathway in non-obese diabetic (NOD) mice.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinska M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RN
 RP PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.

RX MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
 RA Wen Z., Zhong Z., Darnell J.E. Jr.;
 RT "Maximal activation of transcription by Stat1 and Stat3 requires both
 RT tyrosine and serine phosphorylation.";
 RL Cell 82:241-250(1995).
 RN [9]
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
 RX MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
 RA Becker S., Groner B., Mueller C.W.;
 RT "Three-dimensional structure of the Stat3beta homodimer bound to
 RT DNA.";
 RL Nature 394:145-151(1998).
 CC
 CC -|- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes. STAT3B interacts with the N-terminal
 CC part of JUN to activate such promoters in a cooperative way.
 CC -|- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -|- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL (By similarity).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation.
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=Stat3A;
 CC IsoId=P42227-1; Sequence=Displayed;
 CC Name=Stat3B;
 CC IsoId=P42227-2; Sequence=VSP_006287;
 CC Name=Del-701;
 CC IsoId=P42227-3; Sequence=VSP_010475;
 CC -|- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
 CC kidney. STAT3B is also detected in the liver, although in a much
 CC less abundant manner.
 CC -|- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity (By similarity).
 CC -|- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -|- SIMILARITY: Contains 1 SH2 domain.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL; L29278; AAA37254.1; --
 CC EMBL; U06922; AAA19452.1; --
 CC EMBL; U08378; AAA56668.1; --
 CC EMBL; U30709; AAC52612.1; --
 CC EMBL; AF246978; AAL59017.1; --
 CC EMBL; AY299489; AAQ75418.1; --
 CC EMBL; AY299490; AAQ75419.1; --
 CC EMBL; BC003806; AAH03806.1; --
 CC FIR; I49508; I49508.
 CC PDB; 1BG1; X-ray; A=1-722.
 CC TRANSFAC; T01574; --
 CC MGD; MGI:103038; Stat3.
 CC GO; GO:0005737; Cytoplasm; IDA.
 CC GO; GO:0005634; C:nucleus; IDA.
 CC GO; GO:0005886; C:plasma membrane; IDA.
 CC GO; GO:0003677; F:DNA binding; IDA.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC GO; GO:0018563; F:transcriptional activator activity; IDA.
 CC GO; GO:0007259; P:JAK-STAT cascade; IDA.
 CC GO; GO:0006357; P:regulation of transcription from Pol II pro. .; IDA.
 CC InterPro; IPR008967; P53 like_DNA_bnd.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001217; STAT.
 CC Pfam; PF00017; SH2; 1.
 CC Pfam; PF01017; STAT_alpha; 1.
 CC Pfam; PF02864; STAT_bind; 1.

STA3_BOVIN STANDARD; PRT; 770 AA.
 ID STA3_BOVIN STANDARD; PRT; 770 AA.
 AC P61635;
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DE Signal transducer and activator of transcription 3.
 DE Signal transducer and activator of transcription 3.
 DE Signal transducer and activator of transcription 3.
 GN Name=STAT3;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
 RT "The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus
 during ruminant evolution.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
 (IL-6)-responsive elements identified in the promoters of various
 acute-phase protein genes (By similarity).
 CC -1- PATHWAY: Involved in the gpl30-mediated signaling pathway.
 CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 member (at least STAT1). Interacts with NCOAL (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 in response to phosphorylation (By similarity).
 CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AJ620655; CAP06182.1; .
 DR PROSITE; P55001; SH2; 1
 KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
 KW Transcription regulation.
 FT DOMAIN 580 670 SH2.
 FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 FT MOD_RES 727 727 Phosphoserine (By similarity).
 SQ SEQUENCE 770 AA; 87974 MW; 9CEB147C73E83274 CRC64;
 Query Match 97.3%; Score 1137; DB 1; Length 770;
 Best Local Similarity 97.4%; Pred. No. 1.1e-61;
 Matches 223; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQMLEQHLQDVRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 DB 130 NHPTAAVTEKQMLEQHLQDVRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQMKQMLEQMLTALDQMRRSIVSELGALLSAMEYVQKTLTDEELADWKRPEI 120
 DB 190 GNNQSVTRQMKQMLEQMLTALDQMRRSIVSELGALLSAMEYVQKTLTDEELADWKRPEI 249
 QY 121 ACIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKVKSGDPIVQHRPMLERI 180
 DB 250 ACIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKVKSGDPIVQHRPMLERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALLVKFPPEL 229
 DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALLVKFPPEL 358
 RESULT 5
 Q6DV79
 ID Q6DV79 PRELIMINARY; PRT; 771 AA.
 AC Q6DV79;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Signal transducer and activator of transcription 3.
 DE Signal transducer and activator of transcription 3.
 DE Signal transducer and activator of transcription 3.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou G.Y., Leung F.C.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY641397; AAT64887.1; .
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1
 DR Pfam; PF01017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR PROSITE; P55001; SH2; 1.
 SQ SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;
 Query Match 95.7%; Score 1119; DB 2; Length 771;
 Best Local Similarity 96.1%; Pred. No. 1.5e-60;
 Matches 219; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 QY 2 HPTAAVTEKQMLEQHLQDVRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 61
 DB 131 HPTAAVTEKQMLEQHLQDVRKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 190
 QY 62 NNSQSVTRQMKQMLEQMLTALDQMRRSIVSELGALLSAMEYVQKTLTDEELADWKRPEIA 121
 DB 191 NNSQSVTRQMKQMLEQMLTALDQMRRSIVSELGALLSAMEYVQKTLTDEELADWKRPEIA 250
 QY 122 CIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKVKSGDPIVQHRPMLERI 181
 DB 251 CIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKVKSGDPIVQHRPMLERI 310
 QY 182 ELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALLVKFPPEL 229
 DB 311 ELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFATAVALLVKFPPEL 358
 RESULT 6
 Q9PVX8 PRELIMINARY; PRT; 769 AA.
 ID Q9PVX8 PRELIMINARY; PRT; 769 AA.
 AC Q9PVX8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Stat 3.
 GN Name=stat 3;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
 RA Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
 RA Asashima M., Yokota T.;
 RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
 RT embryos independent of BMP-4.";
 RL Dev. Biol. 216:481-490 (1999).
 DR EMBL; AB017701; BAA86061.1; .

2

CC Acanthomorpha; Acanthopterygii; to the EMBL/GenBank/DBJ databases.
 OC Beloniformes; Adrianichthyidae; Oryziinae; Atherinomorpha;
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu R., Hong Y.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY639947; AAT64912.1; -;
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0004871; F:signal transducer activity; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO: GO:0006325; P:intracellular signaling cascade; IEA.
 DR GO: GO:0006742; P:intracellular signaling cascade; IEA.
 DR InterPro: IPR008967; P53_like_DNA_bnd.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001217; STAT.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF01017; STAT_alpha; 1.
 DR Pfam: PF02864; STAT_bind; 1.
 DR Pfam: PF02865; STAT_int; 1.
 DR PROSITE: PS5001; SH2; 1.
 DR PROSITE: PS5001; SH2; 1.
 SQ SEQUENCE 765 AA; 87566 MW; F5D01408748EC703 CRC64;

Query Match 85.4%; Score 998; DB 2; Length 765;
 Best Local Similarity 83.5%; Pred. No. 3.8e-53;
 Matches 192; Conservative 20; Mismatches 16; Indels 2; Gaps 2

Qy 2 HPTAAVTEKQOMLEQHLQDYRKVEQDLLEQKMKVVENLQDDPFDNYKTLKSGDM-QDLN 60
 Db 130 HPTGVVTEKQOILHNLQDIRKRVQDMEQKMKLENLQDDPFDNYKTLKSGQLNQDLN 189
 Qy 61 GNNO-SVTRQKQOOLEOMLTALDQWRRSIVSELGLLSAMEYVQKTLTDEELADWKRRPE 119
 Db 190 GNSQAATRQKQAKLEQMLSDQLRQIVTEMGGLLTAMDYVQKNLTDEELADWKRRQ 249
 Qy 120 IACIGGPNICLDRLNWTITSLAESQLQTRQOIKKLELQKQSVKGDPIVQHRPMLER 179
 Db 250 IACIGGPNICLDRLWTITSLAESQLQIRQOIKKLELQKQSVKGDPIIQRPALEBK 359
 Qy 180 IVELFRNLKSAFVVERQPCMPMPDRPLVIKTGVQFATAVALLKFPPEL 229
 Db 310 IVDLFRNLKSAFVVERQPCMPMPDRPLVIKTGVQFTNKVRLLVKFPPEL 359

RESULT 10
 Q6GUE7 PRELIMINARY; PRT; 785 AA.
 ID Q6GUE7
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Signal transducer and activator of transcription 3 isoform 1.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu R., Hong Y.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY641434; AAT46364.1; -;
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0004871; F:signal transducer activity; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006325; P:intracellular signaling cascade; IEA.
 DR GO: GO:0006742; P:intracellular signaling cascade; IEA.
 DR InterPro: IPR008967; P53_like_DNA_bnd.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001217; STAT.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF01017; STAT_alpha; 1.


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Matches 192; Conservative 21; Mismatches 15; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHLQDVRRVQDLQKMKVVENLQDDFDNFYKTLKSQDGM-QDLN 60
Db 130 HPTGTVTEKQMLEHNLQDQIRKRVQDMQKMLENLQDDFDNFYKTLKSAGELSQDLN 189
QY 61 GNNQ-SVTRQKMQOLEMLTALDQMRISIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEQMLSDQLRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLENWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLEWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 13
QY0Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF3071106; AAL09415.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00117; SH2; 1.
DR Pfam; PF02864; STAT_alpha; 1.
DR Pfam; PF02865; STAT_bind; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FE18BEFD8BE CRC64;

Query Match 83.3%; Score 974; DB 2; Length 764;
Best Local Similarity 82.2%; Pred. No. 1.1e-51;
Matches 189; Conservative 21; Mismatches 18; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHLQDVRRVQDLQKMKVVENLQDDFDNFYKTLKSQDGM-QDLN 60
Db 130 NPSGTVTEKQMLENLQDQIRKRVQDMQKMLENLQDDFDNFYKTLKSQELSQDLN 189
QY 61 GNNQ-SVTRQKMQOLEMLTALDQMRISIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEQMLSDQLRRQIVTEMAGLLTAMDYVQKNTLDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLENWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLEWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 14
QY0Y16 PRELIMINARY; PRT; 767 AA.
AC Q13133;
DT 01-JUL-1997 (TEMBLrel. 04, Created)
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE STAT3.
GN Names=rbtStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AAB60926.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;

Query Match 82.5%; Score 964; DB 2; Length 767;
Best Local Similarity 80.1%; Pred. No. 4.6e-51;
Matches 185; Conservative 25; Mismatches 19; Indels 2; Gaps 2;
QY 1 NHPTAAVTEKQMLEQHLQDVRRVQDLQKMKVVENLQDDFDNFYKTLKSQDGM-QDL 59
Db 129 SHPSGTVTEKQMLEHNLQDQIRKRVQDMQKMLENLQDDFDNFYKTLKSQELSQDM 188
QY 60 GNNQ-SVTRQKMQOLEMLTALDQMRISIVSELAGLLSAMEYVQKTLTDEELADWKRRP 118
Db 189 NGNSQAARQKMAQLEQMLSDQLRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 248
QY 119 ETACIGGPPNICLDRLENWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 178
Db 249 QIACIGGPPNICLDRLEWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 308
QY 179 RIVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 309 KIVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 15
QY0Y16 PRELIMINARY; PRT; 163 AA.
AC Q9N145;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Signal transducer and activator of transcription (Fragment).
GN Names=STAT3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
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Matches 192; Conservative 21; Mismatches 15; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHLQDVRRVQDLQKMKVVENLQDDFDNFYKTLKSQDGM-QDLN 60
Db 130 HPTGTVTEKQMLEHNLQDQIRKRVQDMQKMLENLQDDFDNFYKTLKSAGELSQDLN 189
QY 61 GNNQ-SVTRQKMQOLEMLTALDQMRISIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEQMLSDQLRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLENWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLEWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 13
QY0Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF3071106; AAL09415.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00117; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FE18BEFD8BE CRC64;

Query Match 83.3%; Score 974; DB 2; Length 764;
Best Local Similarity 82.2%; Pred. No. 1.1e-51;
Matches 189; Conservative 21; Mismatches 18; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHLQDVRRVQDLQKMKVVENLQDDFDNFYKTLKSQDGM-QDLN 60
Db 130 NPSGTVTEKQMLENLQDQIRKRVQDMQKMLENLQDDFDNFYKTLKSQELSQDLN 189
QY 61 GNNQ-SVTRQKMQOLEMLTALDQMRISIVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEQMLSDQLRRQIVTEMAGLLTAMDYVQKNTLDEELADWKRRQ 249
QY 120 IACIGGPPNICLDRLENWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLEWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 14
QY0Y16 PRELIMINARY; PRT; 767 AA.
AC Q13133;
DT 01-JUL-1997 (TEMBLrel. 04, Created)
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE STAT3.
GN Names=rbtStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AAB60926.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;

Query Match 82.5%; Score 964; DB 2; Length 767;
Best Local Similarity 80.1%; Pred. No. 4.6e-51;
Matches 185; Conservative 25; Mismatches 19; Indels 2; Gaps 2;
QY 1 NHPTAAVTEKQMLEQHLQDVRRVQDLQKMKVVENLQDDFDNFYKTLKSQDGM-QDL 59
Db 129 SHPSGTVTEKQMLEHNLQDQIRKRVQDMQKMLENLQDDFDNFYKTLKSQELSQDM 188
QY 60 GNNQ-SVTRQKMQOLEMLTALDQMRISIVSELAGLLSAMEYVQKTLTDEELADWKRRP 118
Db 189 NGNSQAARQKMAQLEQMLSDQLRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 248
QY 119 ETACIGGPPNICLDRLENWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 178
Db 249 QIACIGGPPNICLDRLEWITSLSAESQLQTRQIKKLEELQKQSYKGDPIVQHRPMLER 308
QY 179 RIVELFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 229
Db 309 KIVDLFRNLKMSAFVVERQPCMPHDPRLPVIKTGQVFATAVALLVKFPPEL 359

RESULT 15
QY0Y16 PRELIMINARY; PRT; 163 AA.
AC Q9N145;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Signal transducer and activator of transcription (Fragment).
GN Names=STAT3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
```

DR EMBL; AF227560; AAF73401.1; -.
DR HSSP; P42227; IBGI.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; PS3_like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
FT NON_TER 1 163
SQ SEQUENCE 163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;

Query Match 54.7%; Score 639; DB 2; Length 163;
Best Local Similarity 96.1%; Pred. No. 6.9e-32;
Matches 123; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 102 VQKTLTDEELADWKRRPEIACIGGPPNICLDRLNNWITSLSAESQLOTRQOIKKLEELQOK 161
DB 1 VQKTLTDEELADWKRRQIACIGGPPNICLDRLNNWITSLSAESQLOTRQOIKKLEELQOK 60

QY 162 VSYKGDPIVQHRPMLERIVELEFRLMKSAFVVERQPCMPMHDPDRPLVIKTVGVQFATAVA 221
DB 61 VSYKGDPIVQHRPMLERIVELEFRLMKSAFVVERQPCMPMHDPDRPLVIKTVGVQFATAVA 120

QY 222 LLVKFPPEL 229
DB 121 LLVKFPPEL 128

Search completed: May 25, 2005, 17:43:43
Job time : 96.284 secs

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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:14:45 ; Search time 121.891 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-30

Perfect score: 1172
Sequence: 1 NPTAAVTEKQMLEQHAQ.....IKTGVOFTKVRLLVKFPPEL 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq19808:*
- 2: Geneseq19908:*
- 3: Geneseq20008:*
- 4: Geneseq20018:*
- 5: Geneseq20028:*
- 6: Geneseq20038:*
- 7: Geneseq20038s:*
- 8: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1172	100.0	229	4 AAY72862	Aay72862 Mouse Sta
2	1167	99.6	229	4 AAY72850	Aay72850 Mouse Sta
3	1167	99.6	252	4 AAY72846	Aay72846 Mouse Sta
4	1167	99.6	271	4 AAY72841	Aay72841 Mouse Sta
5	1167	99.6	770	2 AAY72082	Aay72082 Mouse Sta
6	1167	99.6	770	2 AAW03176	Aaw03176 Mouse Sta
7	1163	99.2	229	4 AAY72863	Aay72863 Mouse Sta
8	1156	98.6	720	5 AAE22055	Aae22055 Human Sta
9	1156	98.6	769	5 ABB57164	Abb57164 Mouse isc
10	1156	98.6	769	5 AAE22054	Aae22054 Human Sta
11	1156	98.6	769	5 AAE22056	Aae22056 Human pro
12	1156	98.6	770	2 AAR82295	Aar82295 Mouse liv
13	1156	98.6	770	2 AAY03768	Aay03768 Human STA
14	1156	98.6	770	3 AAB12377	Aab12377 N-termina
15	1156	98.6	770	5 AAE14652	Aae14652 Murine ST
16	1156	98.6	770	5 ABG69497	Abg69497 Human bai
17	1156	98.6	770	6 ABU10476	Abu10476 Mouse STA
18	1156	98.6	770	8 ADN04365	Adn04365 Antipeori
19	1156	98.6	770	8 ADP54789	Adp54789 Human PRO
20	1156	98.6	793	3 AAB58442	Aab58442 Lung canc
21	1153	98.4	770	7 ADD44738	Add44738 Rat Prote
22	1152.5	98.3	228	4 AAY72861	Aay72861 Mouse Sta
23	1151	98.2	229	4 AAY72860	Aay72860 Mouse Sta
24	1151	98.2	770	2 AAR82293	Aar82293 Human pia
25	1151	98.2	770	4 AAB19964	Aab19964 Human sig

26	1151	98.2	770	5 AAE15174	Aae15174 Human Sta
27	1151	98.2	770	7 ADD44740	Add44740 Human Pro
28	1089	92.9	213	4 AAY72851	Aay72851 Mouse Sta
29	1089	92.9	236	4 AAY72847	Aay72847 Mouse Sta
30	1044	89.1	223	4 AAY72854	Aay72854 Mouse Sta
31	845	72.1	185	4 AAY72855	Aay72855 Mouse Sta
32	776	66.2	176	4 AAY72848	Aay72848 Mouse Sta
33	653	55.7	128	4 AAY72852	Aay72852 Mouse Sta
34	600	51.2	143	4 AAY72849	Aay72849 Mouse Sta
35	576	49.1	749	5 AAG78526	Aag78526 Rat STAT-
36	572	48.8	268	4 AAY72844	Aay72844 Mouse Sta
37	572	48.8	582	2 AAW62996	Aaw62996 Human tru
38	572	48.8	582	6 ABU04748	Abu04748 Human exp
39	572	48.8	582	8 ADH57036	Adh57036 Truncated
40	572	48.8	680	6 ABR59713	Abr59713 Human sig
41	572	48.8	712	2 AAR72079	Aar72079 Human Sta
42	572	48.8	712	2 AAW03170	Aaw03170 Human STA
43	572	48.8	712	2 AAW62995	Aaw62995 Human Sta
44	572	48.8	712	6 ABU04747	Abu04747 Human exp
45	572	48.8	712	6 ABU04735	Abu04735 Human exp

ALIGNMENTS

RESULT 1

AAY72862
ID AAY72862 standard; protein; 229 AA.
XX AAY72862;
AC AAY72862;
XX 31-MAY-2001 (first entry)
DT
DE Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy; mutant; mutein.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 1..25
FT /note= "Stat3-c-Jun interaction region 1; corresponds to
130-154 position of Stat3 protein"
FT Misc-difference 19
FT /note= "Wild type Leu substituted with Ala; corresponds
to 148 position of Stat-3 protein"
FT Region 213..229
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
342-358 position of Stat3 protein"

WO200116605-A2.

08-MAR-2001.

30-AUG-2000; 2000WO-US023822.

31-AUG-1999; 99US-00387418.

(UYRQ) UNIV ROCKEFELLER.

Zhang X, Horvath C, Wzrzeszynska MH, Darnell JE;

WPI; 2001-226705/23.

Identifying an agent for use in modulating the interaction between
transcription factor c-Jun and a Stat3 protein.

Claim 66; Page 85; 86pp; English.

The present sequence is mouse Stat3 mutant (L148A) protein fragment
containing 130-358 amino acids of Stat3 protein. This mutant is obtained

CC by replacing Leu 148 with Ala in Stat3 protein. The invention relates to
 CC methods for identifying interacting regions of transcription factors and
 CC methods for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX Sequence 229 AA;

Query Match 100.0%; Score 1172; DB 4; Length 229;
 Best Local Similarity 100.0%; Pred. No. 1.2e-101;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQKQMLEQHAQDVRRKRVQDLEQKMKVVENLQDDDFDNFKTKLSQGDMDLN 60
 DB 1 NHPTAAVVTKEQKQMLEQHAQDVRRKRVQDLEQKMKVVENLQDDDFDNFKTKLSQGDMDLN 60
 QY 61 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLISAMEYVQKTLTDEELADWKRPEI 120
 DB 61 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLISAMEYVQKTLTDEELADWKRPEI 120
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIKKLEELQKVKYKGDPIVQHRPMLERI 180
 DB 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIKKLEELQKVKYKGDPIVQHRPMLERI 180
 QY 181 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPEL 229
 DB 181 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPEL 229

RESULT 2
 AAY72850
 ID AAY72850 standard; protein; 229 AA.
 XX
 AC AAY72850;
 XX
 DT 31-MAY-2001 (first entry)
 DE
 XX Mouse Stat3 protein fragment #8 (130-358 amino acids).

XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX Mus musculus.

XX Key Location/Qualifiers
 FT Region 1..25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 130-154 position of Stat3 protein"
 FT Region 213..229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 342-358 position of Stat3 protein"
 XX WO200116605-A2.

XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.

XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.

XX Claim 65; Page 76-77; 86pp; English.

XX The present sequence is mouse Stat3 protein fragment containing 130-358
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX Sequence 229 AA;

Query Match 99.6%; Score 1167; DB 4; Length 229;
 Best Local Similarity 99.6%; Pred. No. 3.5e-101;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQKQMLEQHAQDVRRKRVQDLEQKMKVVENLQDDDFDNFKTKLSQGDMDLN 60
 DB 1 NHPTAAVVTKEQKQMLEQHLQDVRRKRVQDLEQKMKVVENLQDDDFDNFKTKLSQGDMDLN 60
 QY 61 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLISAMEYVQKTLTDEELADWKRPEI 120
 DB 61 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLISAMEYVQKTLTDEELADWKRPEI 120
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIKKLEELQKVKYKGDPIVQHRPMLERI 180
 DB 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIKKLEELQKVKYKGDPIVQHRPMLERI 180
 QY 181 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPEL 229
 DB 181 VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPEL 229

RESULT 3
 AAY72846
 ID AAY72846 standard; protein; 252 AA.
 XX
 AC AAY72846;
 XX
 DT 31-MAY-2001 (first entry)
 DE
 XX Mouse Stat3 protein fragment #4 (107-358 amino acids).

XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX Mus musculus.

XX Key Location/Qualifiers
 FT Region 24..48
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 130-154 position of Stat3 protein"
 FT Region 236..252
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 342-358 position of Stat3 protein"
 XX WO200116605-A2.

XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;

XX DR WPI; 2001-226705/23.
 XX XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX XX
 XX PS Claim 65; Page 73; 86pp; English.
 XX XX
 CC The present sequence is mouse Stat3 protein fragment containing 107-358
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX SQ Sequence 252 AA;
 Query Match 99.6%; Score 1167; DB 4; Length 252;
 Best Local Similarity 99.6%; Pred. No. 4e-101;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQKQMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 Db 24 NHPTAAVVTKEQKQMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 83
 QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVOKLTLDDELADWKRPEI 120
 Db 84 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVOKLTLDDELADWKRPEI 143
 QY 121 ACIGGPPNICLDRLNWNITSLAESQLQTRQIQKLELOQKVSYKGDPIVQHRPMLERI 180
 Db 144 ACIGGPPNICLDRLNWNITSLAESQLQTRQIQKLELOQKVSYKGDPIVQHRPMLERI 203
 QY 181 VELFRNLMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 204 VELFRNLMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKPPPEL 252
 RESULT 4
 AAY72841
 ID AAY72841 standard; protein; 271 AA.
 AC AAY72841;
 XX XX
 DT 31-MAY-2001 (first entry)
 DE Mouse Stat3 protein fragment #2 (107-377 amino acids).
 XX XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX OS Mus musculus.
 XX XX
 FH Key Location/Qualifiers
 FT Region 24..48
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Region 236..252
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX XX
 PN WO200116605-A2.
 XX XX
 PD 08-MAR-2001.
 XX XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX XX

PR 31-AUG-1999; 99US-00387418.
 XX XX (UVRQ) UNIV ROCKEFELLER.
 XX XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 XX XX
 PT Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.
 XX XX
 PS Claim 65; Page 67-68; 86pp; English.
 XX XX
 CC The present sequence is mouse Stat3 protein fragment containing 107-377
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX SQ Sequence 271 AA;
 Query Match 99.6%; Score 1167; DB 4; Length 271;
 Best Local Similarity 99.6%; Pred. No. 4.4e-101;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQKQMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 Db 24 NHPTAAVVTKEQKQMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 83
 QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVOKLTLDDELADWKRPEI 120
 Db 84 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVOKLTLDDELADWKRPEI 143
 QY 121 ACIGGPPNICLDRLNWNITSLAESQLQTRQIQKLELOQKVSYKGDPIVQHRPMLERI 180
 Db 144 ACIGGPPNICLDRLNWNITSLAESQLQTRQIQKLELOQKVSYKGDPIVQHRPMLERI 203
 QY 181 VELFRNLMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 204 VELFRNLMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKPPPEL 252
 RESULT 5
 AAR72082
 ID AAR72082 standard; protein; 770 AA.
 AC AAR72082;
 XX XX
 DT 25-MAR-2003 (revised)
 DT 27-SEP-1995 (first entry)
 XX XX
 DE Mouse Stat3 (19sf6).
 XX XX
 KW Signal transducer and activator of transcription; STAT; 19sf6; Stat3;
 KW receptor recognition factor; transcription factor; cellular debilitation;
 KW derangement; dysfunction; interferon-gamma.
 XX OS Mus sp.
 XX PN WO9508629-A1.
 XX XX
 PD 30-MAR-1995.
 XX XX
 PF 26-SEP-1994; 94WO-US010849.
 XX XX
 PF 24-SEP-1993; 93US-00126588.
 PR 24-SEP-1993; 93US-00126595.

PR 11-MAR-1994; 94US-00212184.
 PR 11-MAR-1994; 94US-00212185.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
 XX
 DR WPI; 1995-139598/18.
 DR N-PSDB; AAQ89340.
 XX
 PT Receptor recognition factor implicated in transcriptional stimulation of
 PT genes - useful in drug screening assays and/or for treating cellular
 PT debilitations, derangements and/or dysfunctions, etc.
 XX
 PS Claim 1; Page 107-110; 160pp; English.
 XX
 CC A fragment encoding the human Stat91 protein was used to screen a murine
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAQ72080)
 CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
 CC mouse gene as probe, 2 additional members of the 113-91 family of
 CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
 CC -40) were cloned in plasmids 135f1 and 195f6 and encoded proteins termed
 CC Stat4 (AAQ72081) and Stat3 (AAQ72082), respectively. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 770 AA;
 Query Match 99.6%; Score 1167; DB 2; Length 770;
 Best Local Similarity 99.6%; Pred. No. 1.8e-100;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 60
 Db 130 NHPTAAVVTKEQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDEELADWKRRPEI 249
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLELOQKVSYGKGPVQHRPMLLEERI 180
 Db 250 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLELOQKVSYGKGPVQHRPMLLEERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKRPPEL 229
 Db 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKRPPEL 358
 RESULT 6
 AAQ03176
 ID AAQ03176 standard; protein; 770 AA.
 XX
 AC AAQ03176;
 XX
 DT 24-OCT-1996 (first entry)
 XX
 DE Mouse STAT4.
 XX
 KW STAT4; signal transducer and activator of transcription;
 KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
 KW autoimmune disease; antagonist; therapy.
 XX
 OS Mus sp.
 XX
 PH Key Location/Qualifiers
 FT Domain 398...508
 FT /label= DNA binding domain
 FT /note= "Claim 3, page 110"
 XX
 PN W09620954-A2.
 XX
 PD 11-JUL-1996.

XX 28-DEC-1995; 95WO-US017025.
 XX
 PR 06-JAN-1995; 95US-00369796.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Darnell JE, Wen Z, Horvath CM, Zhong Z;
 XX
 DR WPI; 1996-333941/33.
 DR N-PSDB; AAT31280.
 XX
 PT New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,
 PT preventing or treating cellular dysfunction, e.g. oncogenesis,
 PT inflammation, parasitic disease or autoimmunity.
 XX
 PS Disclosure; Page 87-90; 138pp; English.
 XX
 CC Mouse signal transducer and activator of transcription (STAT) protein
 CC STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from
 CC ligand-activated receptor kinase complexes followed by nuclear
 CC translocation and DNA binding to activate transcription. Recombinant
 CC STAT4 can be obt'd. using cDNA clone 195f6 (AAT31278) obt'd. from
 CC splenic/thymic cells. STAT4 includes a DNA-binding domain (see also
 CC AAQ03167) capable of both receptor recognition and message delivery via
 CC DNA binding in a receptor-ligand specific manner. STAT proteins and their
 CC DNA binding domains (see also AAQ03165-75) are useful for screening
 CC antagonists used to inhibit STAT-mediated signal transduction and
 CC activation of transcription
 XX
 SQ Sequence 770 AA;
 Query Match 99.6%; Score 1167; DB 2; Length 770;
 Best Local Similarity 99.6%; Pred. No. 1.8e-100;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 60
 Db 130 NHPTAAVVTKEQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDEELADWKRRPEI 249
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLELOQKVSYGKGPVQHRPMLLEERI 180
 Db 250 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLELOQKVSYGKGPVQHRPMLLEERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKRPPEL 229
 Db 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKRPPEL 358
 RESULT 7
 AAQ72863
 ID AAQ72863 standard; protein; 229 AA.
 XX
 AC AAQ72863;
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids).
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy; mutant; mutein.
 XX
 OS Mus musculus.
 XX
 PH Key Location/Qualifiers
 FT Region 1...25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"

FT Misc-difference 22 /note= "wild type Val substituted with Ala corresponds to
FT 151 position of Stat-3 protein"
FT Region 213..229
FT /note= "Stat3-c-Jun interaction region 2; corresponds to
FT 342-358 position of Stat3 protein"
XX WO200116605-A2.
PN 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023822.
XX 31-AUG-1999; 99US-00387418.
XX (UYRQ) UNIV ROCKEFELLER.
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX Claim 66; Page 86; 86pp; English.
XX
XX The present sequence is mouse Stat3 mutant (V151A) protein fragment
XX containing 130-358 amino acids of Stat3 protein. This mutant is obtained
XX by replacing Val 151 with Ala in Stat3 protein. The invention relates to
XX methods for identifying interacting regions of transcription factors and
XX methods for identifying agents which modulates the interaction between a
XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
XX Stat-3, useful for modulating gene transcription e.g., cellular
XX transformation. These identifying agents are used in the treatment of
XX dysproliferative diseases and also for treating cancer and psoriasis. A
XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
XX binding domain, linker domain, SH2 domain and transactivation domain
XX
XX Sequence 229 AA;
SQ

Query Match 99.2%; Score 1163; DB 4; Length 229;
Best Local Similarity 99.1%; Pred. No. 8.3e-101;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVRRVQDLERQKMKVVENLQDDFDVNYKTLKSGQDMQDLN 60
Db 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLERQKMKVVENLQDDFDVNYKTLKSGQDMQDLN 60

QY 61 GNNQSVTRQKMQOLEQMLTALDQNRISIVSELAGLLSAMYVQKTLTDEBLADWKRPEI 120
Db 61 GNNQSVTRQKMQOLEQMLTALDQNRISIVSELAGLLSAMYVQKTLTDEBLADWKRPEI 120

QY 121 ACITGGPPNICLDRLNWTSLAESOLQTRQOIKKLSELQKVSYGKDPVVOHRPMLERI 180
Db 121 ACITGGPPNICLDRLNWTSLAESOLQTRQOIKKLSELQKVSYGKDPVVOHRPMLERI 180

QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVTKTGQFTTKVRLLVKPEL 229
Db 181 VELFRNLKMSAFVVERQPCMPMPDRPLVTKTGQFTTKVRLLVKPEL 229

RESULT 8
AAE22055
ID AAE22055 standard; protein; 720 AA.
XX AC AAE22055;
XX 25-JUL-2002 (first entry)
XX Human Stat3beta protein.
XX
XX Human; signal transducer and activator of transcription 3; ischaemia;
KW Immune response; Stat3; coronary atherosclerosis; vascular occlusion;

KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
KW shock; chronic active hepatitis; adult respiratory distress syndrome;
KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
KW cirrhosis; hypoproliferative disorder; gene therapy; growth deficiency;
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 713..714 /note= "Encoded by ACA CCA TTC"
FT WO200220032-A1.
XX 14-MAR-2002.
XX 10-SEP-2001; 2001WO-US028254.
XX 08-SEP-2000; 2000US-0231212P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX (UYSP-) UNIV SOUTH FLORIDA.
XX Yu H, Pardoll D, Jove R, Dalton W;
XX WPI; 2002-362218/39.
XX N-PSDB; AAD35086.
XX
XX Modulating angiogenesis and an immune response in an individual, for
XX treating a hypoxic or ischemic condition, comprises administering a
XX compound that modulates the activity of a signal transducer and activator
XX of transcription 3.
XX
XX Disclosure; Page 87-89; 94pp; English.
XX
XX The invention relates to a method of modulating angiogenesis and immune
XX response. Method involves administering to an individual a compound that
XX modulate the activity of signal transducer and activator of transcription
XX 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
XX hypoxic or ischemic condition or disorder which is the result of stroke,
XX ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
XX tissue ischaemia in the lower extremities, infarction, trauma, vascular
XX occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
XX chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
XX epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
XX nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
XX with neovascularisation. Suppressing an immune response is useful for
XX ameliorating a symptom of an autoimmune disease such as systemic lupus
XX erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
XX Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
XX mixed connective tissue disease, primary biliary cirrhosis, pernicious
XX anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
XX gluten-sensitive enteropathy, autoimmune neuropenia, myasthenia gravis,
XX idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
XX disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
XX infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
XX dense deposit disease. The method is useful in preventing or treating
XX specific proliferative and oncogenic disease which includes sarcomas and
XX carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
XX fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
XX hypoproliferative disorders, physical trauma, lesions and wounds. The
XX method is also used in gene therapy. The present sequence is human
XX Stat3beta protein
XX
XX Sequence 720 AA;
SQ

Query Match 98.6%; Score 1156; DB 5; Length 720;
Best Local Similarity 98.7%; Pred. No. 1.8e-99;

Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVKRVQDLEQKMKVVENIQDDDFDNFKYTKLSQGDMDQDLN 60
 DB 130 NHPTAAVTEKQOMLEQHLQDVKRVQDLEQKMKVVENIQDDDFDNFKYTKLSQGDMDQDLN 189
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
 QY 121 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLEELQKVSYGKDPVQHRPMLERI 180
 DB 250 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLEELQKVSYGKDPVQHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229
 DB 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 358

RESULT 9
 ABB57164
 ID ABB57164 standard; protein; 769 AA.
 XX
 AC ABB57164;
 XX
 DT 07-MAR-2002 (first entry)
 XX
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:398.
 XX
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
 OS Mus musculus.
 XX
 PN W0200188188-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-JP004192.
 XX
 PF 18-MAY-2000; 2000JP-00145977.
 XX
 PR (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX
 PA Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX
 PI WPI; 2002-034733/04.
 XX
 DR N-PSDB; ABI99454.
 XX
 XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.

Claim 2; Page 1084-1087; 2690pp; English.
 XX
 XX The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (1) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (1). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX
 SQ Sequence 769 AA;

Query Match 98.6%; Score 1156; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 1.9e-99;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVKRVQDLEQKMKVVENIQDDDFDNFKYTKLSQGDMDQDLN 60
 DB 130 NHPTAAVTEKQOMLEQHLQDVKRVQDLEQKMKVVENIQDDDFDNFKYTKLSQGDMDQDLN 189
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
 QY 121 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLEELQKVSYGKDPVQHRPMLERI 180
 DB 250 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLEELQKVSYGKDPVQHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229
 DB 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 358

RESULT 10
 AAE22054
 ID AAE22054 standard; protein; 769 AA.
 XX
 AC AAE22054;
 XX
 DT 25-JUL-2002 (first entry)
 XX
 DE Human Stat3 protein.
 XX
 KW Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.

Homo sapiens.
 OS
 XX
 PN WO200220032-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US028254.
 XX
 PF 08-SEP-2000; 2000US-0231212P.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 XX Yu H, Pardoll D, Jove R, Dalton W;
 PI WPI; 2002-362218/39.
 XX
 DR N-PSDB; AAD35065.
 XX
 XX Modulating angiogenesis and an immune response in an individual, for
 PT treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.
 XX
 PS Disclosure; Page 83-85; 94pp; English.
 XX
 CC The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing

CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neuropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human Stat3
 CC protein
 CC
 XX
 SQ Sequence 769 AA;

Query Match 98.6%; Score 1156; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 1.9e-99;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDDFNYTKLSQGDMDLN 60
 Db 130 NHPTAAVVTKEQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDDFNYTKLSQGDMDLN 189
 QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDTDELADWKRPEI 120
 Db 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDTDELADWKRPEI 249
 QY 121 ACIGGPPNICDLRLENWITSLSAQLOTRQIKKLELOQKVSYGKGDPIVQHRPMLERI 180
 Db 250 ACIGGPPNICDLRLENWITSLSAQLOTRQIKKLELOQKVSYGKGDPIVQHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPHDPRLVTKGVQTTKRVLLVKPEL 229
 Db 310 VELFRNLMSAFVVERQPCMPHDPRLVTKGVQTTKRVLLVKPEL 358

RESULT 11
 AAE22056
 ID AAE22056 standard; protein; 769 AA.

XX AAE22056;

XX 25-JUL-2002 (first entry)

XX Human protein related to angiogenesis regulation.

XX Human; signal transducer and activator of transcription 3; ischaemia;
 KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
 KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
 KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
 KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
 KW shock; chronic active hepatitis; adult respiratory distress syndrome;
 KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
 KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
 KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
 KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
 KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
 KW cirrhosis; hypoproliferative disorder; lesion.

XX Homo sapiens.

XX

PN WO200220032-A1.
 XX 14-MAR-2002.
 PD 10-SEP-2001; 2001WO-US028254.
 PF 08-SEP-2000; 2000US-0231212P.
 PR (UYJO) UNIV JOHNS HOPKINS.
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX Yu H, Pardoll D, Jove R, Dalton W;
 XX WPI; 2002-362218/39.
 DR Modulating angiogenesis and an immune response in an individual, for
 XX treating a hypoxic or ischemic condition, comprises administering a
 PT compound that modulates the activity of a signal transducer and activator
 PT of transcription 3.
 XX
 PS Disclosure; Page 83-85; 94pp; English.

XX The invention relates to a method of modulating angiogenesis and immune
 CC response. Method involves administering to an individual a compound that
 CC modulate the activity of signal transducer and activator of transcription
 CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing
 CC hypoxic or ischaemic condition or disorder which is the result of stroke,
 CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
 CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
 CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
 CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
 CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
 CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
 CC with neovascularisation. Suppressing an immune response is useful for
 CC ameliorating a symptom of an autoimmune disease such as systemic lupus
 CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
 CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
 CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
 CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
 CC gluten-sensitive enteropathy, autoimmune neuropenia, myasthenia gravis,
 CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
 CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
 CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
 CC dense deposit disease. The method is useful in preventing or treating
 CC specific proliferative and oncogenic disease which includes sarcomas and
 CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
 CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
 CC hypoproliferative disorders, physical trauma, lesions and wounds. The
 CC method is also used in gene therapy. The present sequence is human
 CC protein related to angiogenesis regulation
 XX
 SQ Sequence 769 AA;

Query Match 98.6%; Score 1156; DB 5; Length 769;
 Best Local Similarity 98.7%; Pred. No. 1.9e-99;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDDFNYTKLSQGDMDLN 60
 Db 130 NHPTAAVVTKEQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDDFNYTKLSQGDMDLN 189
 QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDTDELADWKRPEI 120
 Db 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDTDELADWKRPEI 249
 QY 121 ACIGGPPNICDLRLENWITSLSAQLOTRQIKKLELOQKVSYGKGDPIVQHRPMLERI 180
 Db 250 ACIGGPPNICDLRLENWITSLSAQLOTRQIKKLELOQKVSYGKGDPIVQHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPHDPRLVTKGVQTTKRVLLVKPEL 229
 Db 310 VELFRNLMSAFVVERQPCMPHDPRLVTKGVQTTKRVLLVKPEL 358

RESULT 12

AAR82995
ID AAR82995 standard; protein; 770 AA.

XX
AC AAR82995;

XX
DT 25-MAR-1996 (first entry)

XX
DE Mouse liver acute phase response factor.

XX
KW Mouse; acute phase response factor; transcription factor; interleukin-6;
KW signal transduction; liver; antibody; antisense; ribozyme;
KW antiinflammatory; antitumor; hypotensive; therapy.

XX
OS Mus musculus.

XX
PN EP676469-A2.

XX
PD 11-OCT-1995.

XX
PF 29-MAR-1995; 95EP-00104670.

XX
PR 04-APR-1994; 94JP-00065825.

XX
PA (KISH/) KISHIMOTO T.

XX
PI Akira S, Kishimoto T;

XX
DR WPI; 1995-346089/45.

XX
DR N-PSDB; AAT05619.

XX
PT New acute phase response factor - for developing inhibitory agents for
PT treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
PT diseases.

XX
PS Claim 10; Page 20-22; 31pp; English.

XX
CC The sequence represents a mouse acute phase response factor (APRF), a
CC transcription factor related to signal transduction of interleukin-6 (IL-
CC 6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
CC library using a polymerase chain reaction product (amplified using
CC primers derived from an IL-6-treated mouse liver peptide) as a probe.
CC APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
CC ribozymes, may be used to treat diseases induced by IL-6, e.g.
CC inflammatory disease, leukemia, cancer, osteoclastia, pulmonary
CC hypertension, etc

XX
SQ Sequence 770 AA;

Query Match 98.6%; Score 1156; DB 2; Length 770;

Best Local Similarity 98.7%; Pred. No. 1.9e-99;

Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60

DB 130 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

DB 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGGPNICLDRLNNITSLAESOLQTRQIKKLELQKVS YKGDPIVQHRPMLERI 180

DB 250 ACIGGPNICLDRLNNITSLAESOLQTRQIKKLELQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 13

AAY03768

ID AAY03768 standard; protein; 770 AA.

XX
AC AAY03768;

XX
DT 11-JUN-1999 (first entry)

XX
DE Human STAT3 allelic variant.

XX
KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;
KW intracellular transcription factor; interleukin-6; medicament; variant;
KW pharmaceutical; autoimmune disease; inflammatory; human.

XX
OS Homo sapiens.

XX
PN EP905234-A2.

XX
PD 31-MAR-1999.

XX
PF 18-FEB-1998; 98EP-00102774.

XX
PR 16-SEP-1997; 97EP-00116061.

XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

XX
PI Serlupi-Crescenzi O, Della Pietra L;

XX
DR WPI; 1999-192664/17.

XX
DR N-PSDB; AAY29281.

XX
PT New human Signal Transducer and Activator of Transcription 3 (STAT3)
PT allelic variant useful for treatment of autoimmune and inflammatory
PT disease.

XX
PS Claim 2; Page 9-13; 32pp; English.

XX
CC The present sequence represents a predominant allelic variant of human
CC Signal Transducer and Activator of Transcription 3 (STAT3) protein, an
CC intracellular transcription factor which mediates IL-6 signals. The
CC encoding sequence differs from the original published human STAT3 gene
CC sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3
CC DNA molecule can be used for the recombinant expression of the variant.
CC STAT3 protein is useful as a medicament or pharmaceutical composition for
CC treatment of autoimmune or inflammatory diseases

XX
SQ Sequence 770 AA;

Query Match 98.6%; Score 1156; DB 2; Length 770;

Best Local Similarity 98.7%; Pred. No. 1.9e-99;

Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60

DB 130 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

DB 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGGPNICLDRLNNITSLAESOLQTRQIKKLELQKVS YKGDPIVQHRPMLERI 180

DB 250 ACIGGPNICLDRLNNITSLAESOLQTRQIKKLELQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 14

AAB12377

ID AAB12377 standard; peptide; 770 AA.

XX
AC AAB12377;

XX
XX

08-NOV-2000 (first entry)

N-terminal domain of murine STAT-3 protein.

STAT; signal transducer and activator of transcription; crystal; drug design; murine.

Mus sp.

Key Location/Qualifiers

Region 4..9

FT /label= Alpha helix 1

Region 12..21

FT /label= Alpha helix 2

Region 19..21

FT /label= 3(10) helix of alpha helix 2

Region 28..33

FT /label= Alpha helix 3

Region 35..40

FT /label= Alpha helix 4

Region 43..47

FT /label= Alpha helix 5

Region 50..73

FT /label= Alpha helix 6

Region 77..96

FT /label= Alpha helix 7

Region 99..119

FT /label= Alpha helix 8

US6087478-A.

11-JUL-2000.

23-JAN-1998; 98US-00012710.

23-JAN-1998; 98US-00012710.

(UYRQ) UNIV ROCKEFELLER.

Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J; WPI; 2000-505108/45.

New crystals of an N-terminal fragment of a signal transducer and activator of transcription that effectively diffracts x-rays, useful for drug screening and development.

Disclosure; Fig 1; 42pp; English.

The present invention relates to a crystal of an N-terminal fragment of a signal transducer and activator of transcription (STAT) protein. The crystal effectively diffracts x-rays, allowing the determination of the atomic coordinates of the N-terminal domain to a resolution of greater than 5.0 Angstroms. The present sequence is the N-terminal domain of the murine STAT 3 protein. The N-terminal domain enables STAT dimers to interact and bind DNA cooperatively, a mechanism important for gene activation. The crystals are useful in drug screening and development by selecting a potential drug by performing rational drug design with the 3-dimensional structure determined for the crystal

Sequence 770 AA;

Query Match 98.6%; Score 1156; DB 3; Length 770;

Best Local Similarity 98.7%; Pred. No. 1.9e-99;

Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLSQHAQVVRKRVQDLEQRKVVENLQDDFDNFYKTLKSGQDMQDLN 60

DB 130 NHPTAAVTEKQOMLEQLQDVRKRVQDLEQRKVVENLQDDFDNFYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKQOQLQOMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDELDWKRRPEI 120

DB 190 GNNQSVTRQKQOQLQOMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDELDWKRRQOI 249

QY 121 ACIGGPNICLDLENWITSLAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 180

DB 250 ACIGGPNICLDLENWITSLAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVIKTVQFTTKVRLLVKFPPEL 229

DB 310 VELFRNLKMSAFVVERQPCMPMPDRPLVIKTVQFTTKVRLLVKFPPEL 358

RESULT 15

AAE14652

ID AAE14652 standard; protein; 770 AA.

XX AAE14652;

XX 16-JUL-2002 (first entry)

XX Murine STAT3 protein.

XX Signal transducer and activator of transcription; STAT3; drug development; drug discovery; crystal; inflammation; allergy; asthma; leukemia; anaemia; neutropaenia; thrombocytopaenia; cancer; obesity; viral disease; growth retardation; murine.

XX Mus sp.

XX Key Location/Qualifiers

FT Domain 1..130

FT /note= "Conserved N-terminal domain of the STAT family"

XX US6312887-B1.

XX 06-NOV-2001.

XX 24-APR-2000; 2000US-00556273.

XX 23-JAN-1998; 98US-00012710.

XX (UYRQ) UNIV ROCKEFELLER.

XX Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J; WPI; 2002-033337/04.

XX Identifying compounds that bind to signal transducer and activator of transcription proteins, useful for the production of new drugs.

XX Example; Col 47-50; 44pp; English.

XX The invention relates to methods for detecting compounds that bind to signal transducer and activator of transcription (STAT) proteins for the discovery and development of new drug compounds based on the structural properties of the protein crystal. The methods include: identifying a compound that binds to the N-terminal domain of a STAT protein, identifying a compound that enhances or diminishes the binding of the dimeric STAT proteins to each other and/or their nucleic acid binding site; or identifying a compound that enhances or diminishes the ability of STAT protein dimers to induce the expression of a gene operably under the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new drugs. An antagonist of STAT N-terminal dimeric interactions that inhibits the binding of the STAT dimers to adjacent weak binding sites on a promoter of a gene, could be useful as drugs in the treatment of diseases, e.g. inflammation, allergy, asthma and leukaemias. On the other hand, an agonist of N-terminal dimeric interactions between STAT dimers, can be used as drugs in the treatment of diseases e.g. anaemia, neutropaenia, thrombocytopaenia, cancer, obesity, viral diseases and growth retardation. The present sequence is murine STAT3 protein

XX Sequence 770 AA;

Query Match 98.6%; Score 1156; DB 5; Length 770;

Best Local Similarity 98.7%; Pred. NO. 1.9e-99;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	NHPTAAVTEKQOMLEQHAQDVVKRVQDLEQKMKVVENLQDDPFDNYKTKSQGDMODLN	60
Db	130	NHPTAAVTEKQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDPFDNYKTKSQGDMODLN	189
QY	61	GNNQSVTRQKMOLEQMLTALDOMRSIVSELAGLLSAMEYVOKTLTDEELADWKRPEI	120
Db	190	GNNQSVTRQKMOLEQMLTALDOMRSIVSELAGLLSAMEYVOKTLTDEELADWKRQOI	249
QY	121	ACIGGPPNICLDLENWITSLAESQLQTRQIQKKEELOQKVSYPKGDPIVQHRPMLLEERI	180
Db	250	ACIGGPPNICLDLENWITSLAESQLQTRQIQKKEELOQKVSYPKGDPIVQHRPMLLEERI	309
QY	181	VELFRNLKSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPPPEL	229
Db	310	VELFRNLKSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPPPEL	358

Search completed: May 25, 2005, 17:36:38
Job time : 123.057 secs

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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 28.6534 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-30
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQOMLEQHAQ.....IKTGVQFTTKVRLLVKPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/protdata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/protdata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/protdata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/protdata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/protdata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/protdata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1172	100.0	229	3	US-09-387-418A-30
2	1167	99.6	229	3	US-09-387-418A-18
3	1167	99.6	229	3	US-09-387-418A-28
4	1167	99.6	252	3	US-09-387-418A-14
5	1167	99.6	271	3	US-09-387-418A-9
6	1167	99.6	770	1	US-08-369-796-12
7	1167	99.6	770	2	US-08-852-091-12
8	1167	99.6	770	2	US-08-820-754-12
9	1167	99.6	770	3	US-08-956-652-12
10	1167	99.6	770	3	US-08-956-869-12
11	1167	99.6	770	3	US-08-948-547-12
12	1167	99.6	770	3	US-09-364-970-3
13	1167	99.6	770	3	US-09-364-970-5
14	1167	99.6	770	3	US-08-956-653A-12
15	1167	99.6	770	4	US-08-212-185-12
16	1167	99.6	770	5	PCT-US95-17025-12
17	1163	99.2	229	3	US-09-387-418A-31
18	1156	98.6	770	1	US-08-416-581B-9
19	1156	98.6	770	3	US-09-012-710-8
20	1156	98.6	770	3	US-09-556-273-8
21	1156	98.6	770	3	US-09-526-542-2
22	1156	98.6	770	4	US-10-117-087-2
23	1151	98.2	770	1	US-08-416-581B-1
24	1151	98.2	770	1	US-08-416-581B-5
25	1151	98.2	770	3	US-09-087-465-6
26	1151	98.2	770	4	US-09-972-800A-6
27	1151	98.2	771	1	US-08-276-099A-14

28	1151	98.2	771	1	US-08-781-890-14	Sequence 14, Appl
29	1150	98.1	229	3	US-09-387-418A-29	Sequence 29, Appl
30	1089	92.9	213	3	US-09-387-418A-19	Sequence 19, Appl
31	1089	92.9	236	3	US-09-387-418A-15	Sequence 15, Appl
32	1044	89.1	223	3	US-09-387-418A-22	Sequence 22, Appl
33	845	72.1	185	3	US-09-387-418A-23	Sequence 23, Appl
34	776	66.2	176	3	US-09-387-418A-16	Sequence 16, Appl
35	653	55.7	128	3	US-09-387-418A-20	Sequence 20, Appl
36	600	51.2	143	3	US-09-387-418A-17	Sequence 17, Appl
37	572	48.8	268	3	US-09-387-418A-12	Sequence 12, Appl
38	572	48.8	592	4	US-09-430-806A-3	Sequence 3, Appl
39	572	48.8	712	1	US-08-369-796-6	Sequence 6, Appl
40	572	48.8	712	2	US-08-852-091-6	Sequence 6, Appl
41	572	48.8	712	2	US-08-820-754-6	Sequence 6, Appl
42	572	48.8	712	3	US-08-956-652-6	Sequence 6, Appl
43	572	48.8	712	3	US-08-956-869-6	Sequence 6, Appl
44	572	48.8	712	3	US-08-948-547-6	Sequence 6, Appl
45	572	48.8	712	3	US-08-956-653A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-387-418A-30
; Sequence 30, Application US/09387418A
; Patent No. 6391572

; GENERAL INFORMATION:

; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzesczynska, Melissa H

; APPLICANT: Horvath, Curt M

; APPLICANT: Darnell Jr., James E

; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR

; TITLE OF INVENTION: INTERACTIONS

; FILE REFERENCE: 600-1-253

; CURRENT APPLICATION NUMBER: US/09/387,418A

; CURRENT FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 30

; TYPE: PRT

; ORGANISM: Mus musculus

; US-09-387-418A-30

Query Match 100.0%; Score 1172; DB 3; Length 229;

Best Local Similarity 100.0%; Pred. No. 1e-97; Indels 0; Gaps 0;

Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 60

Db 1 NHPTAAVTEKQOMLEQHAQDVVKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQDMQDLN 60

QY 61 GNNQSVTRQMKQOQLTALDQMRRSIVSELAGLLSAMEYVQKLTITDEELADWKRRPEI 120

Db 61 GNNQSVTRQMKQOQLTALDQMRRSIVSELAGLLSAMEYVQKLTITDEELADWKRRPEI 120

QY 121 ACIGGPNICLDRLENNITSLAESQLOTRQOIKKLELOKVSYGKGPVVOHRPMLERI 180

Db 121 ACIGGPNICLDRLENNITSLAESQLOTRQOIKKLELOKVSYGKGPVVOHRPMLERI 180

QY 181 VELFRNLMSAFVVERQPCWMPHDPRLVIKTGVQFTTKVRLLVKPEL 229

Db 181 VELFRNLMSAFVVERQPCWMPHDPRLVIKTGVQFTTKVRLLVKPEL 229

RESULT 2

US-09-387-418A-18

; Sequence 18, Application US/09387418A

; Patent No. 6391572

; GENERAL INFORMATION:

; APPLICANT: Zhang, Xiaokui

; APPLICANT: Wzesczynska, Melissa H

```

; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-18

Query Match      99.6%; Score 1167; DB 3; Length 229;
Best Local Similarity 99.6%; Pred. No. 2.9e-97;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
DB 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60

QY 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

QY 121 ACIGGPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVSYGKDPVVOHRPMLREI 180
DB 121 ACIGGPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVSYGKDPVVOHRPMLREI 180

QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229
DB 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 3
US-09-387-418A-28
; Sequence 28, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-28

Query Match      99.6%; Score 1167; DB 3; Length 229;
Best Local Similarity 99.6%; Pred. No. 2.9e-97;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
DB 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60

QY 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120

QY 121 ACIGGPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVSYGKDPVVOHRPMLREI 180
DB 121 ACIGGPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVSYGKDPVVOHRPMLREI 180

QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229
DB 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 4
US-09-387-418A-14
; Sequence 14, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-14

Query Match      99.6%; Score 1167; DB 3; Length 252;
Best Local Similarity 99.6%; Pred. No. 3.3e-97;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
DB 24 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 83

QY 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 84 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143

QY 121 ACIGGPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVSYGKDPVVOHRPMLREI 180
DB 144 ACIGGPNICLDRLNWTSLAESQLOTRQOIKKLELOQKVSYGKDPVVOHRPMLREI 203

QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229
DB 204 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 252

RESULT 5
US-09-387-418A-9
; Sequence 9, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-9

Query Match      99.6%; Score 1167; DB 3; Length 271;
Best Local Similarity 99.6%; Pred. No. 3.6e-97;

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Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVRRKRVODLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 60
 DB 24 NHPTAAVTEKQOMLEQHAQDVRRKRVODLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 83
 QY 61 GNNQSVTRQKMQOQLTALDQMRRSIVSELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 120
 DB 84 GNNQSVTRQKMQOQLTALDQMRRSIVSELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 143
 QY 121 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 180
 DB 144 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 203
 QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKPEL 229
 DB 204 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKPEL 252

RESULT 6
 US-08-369-796-12
 ; Sequence 12, Application US/08369796
 ; Patent No. 5716622
 ; GENERAL INFORMATION:
 ; APPLICANT: James E. Darnell, Jr.
 ; APPLICANT: Zilong Wen
 ; APPLICANT: Curt M. Horvath
 ; APPLICANT: Zhong Zhong
 ; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
 ; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/08/369,796
 ; FILING DATE: 06-JAN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-116
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-369-796-12

Query Match 99.6%; Score 1167; DB 1; Length 770;
 Best Local Similarity 99.6%; Pred. No. 1.4e-96;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVRRKRVODLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 60
 DB 130 NHPTAAVTEKQOMLEQHAQDVRRKRVODLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQKMQOQLTALDQMRRSIVSELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 120
 DB 130 NHPTAAVTEKQOMLEQHAQDVRRKRVODLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQKMQOQLTALDQMRRSIVSELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 120

DB 190 GNNQSVTRQKMQOQLTALDQMRRSIVSELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 249
 QY 121 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 180
 DB 250 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 309
 QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKPEL 229
 DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKPEL 358

RESULT 7
 US-08-852-091-12
 ; Sequence 12, Application US/08852091
 ; Patent No. 5883228
 ; GENERAL INFORMATION:
 ; APPLICANT: James E. Darnell, Jr.
 ; APPLICANT: Zilong Wen
 ; APPLICANT: Curt M. Horvath
 ; APPLICANT: Zhong Zhong
 ; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
 ; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/08/852,091
 ; FILING DATE: 06-MAY-1997
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/369,796
 ; FILING DATE: 06-JAN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-116
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-852-091-12

Query Match 99.6%; Score 1167; DB 2; Length 770;
 Best Local Similarity 99.6%; Pred. No. 1.4e-96;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVRRKRVODLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 60
 DB 130 NHPTAAVTEKQOMLEQHAQDVRRKRVODLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQKMQOQLTALDQMRRSIVSELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 120
 DB 190 GNNQSVTRQKMQOQLTALDQMRRSIVSELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 249
 QY 121 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 180
 DB 250 ACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVTTKVRLLVKFPPEL 229
 Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVTTKVRLLVKFPPEL 358

RESULT 8
 US-08-754-12
 ; Sequence 12, Application US/08820754
 ; Patent No. 5976835
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan
 ; APPLICANT: Wen, Zilong
 ; APPLICANT: Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/820,754
 ; FILING DATE: 19-MAR-1997
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,185
 ; FILING DATE: 11-MAR-1994
 ; APPLICATION NUMBER: US 07/980,498
 ; FILING DATE: 23-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/854,296
 ; FILING DATE: 19-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO US93/02569
 ; FILING DATE: 19-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/126,588
 ; FILING DATE: 24-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-754-12

Query Match 99.6%; Score 1167; DB 2; Length 770;
 Best Local Similarity 99.6%; Pred. No. 1.4e-96;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQOMLEQHAQDVRKQVQDLEQKMKVVENLODDFNFYKTLKSQGDMDLN 60
 Db 130 NHPTAAVTEKQOMLEQHLQDVRKQVQDLEQKMKVVENLODDFNFYKTLKSQGDMDLN 189

QY 61 GNNQSVTRQKMQOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 Db 190 GNNQSVTRQKMQOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
 QY 121 ACIGGPNICLDRLNWIITSLAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 180
 Db 250 ACIGGPNICLDRLNWIITSLAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVTTKVRLLVKFPPEL 229
 Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQVTTKVRLLVKFPPEL 358

RESULT 9
 US-08-956-652-12
 ; Sequence 12, Application US/08956652
 ; Patent No. 6013475
 ; GENERAL INFORMATION:
 ; APPLICANT: Darnell Jr., James E.
 ; APPLICANT: Schindler, Christian W.
 ; APPLICANT: Fu, Xian-Yuan
 ; APPLICANT: Wen, Zilong
 ; APPLICANT: Zhong, Zhong
 ; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/956,652
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,185
 ; FILING DATE: 11-MAR-1994
 ; APPLICATION NUMBER: US 07/980,498
 ; FILING DATE: 23-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/854,296
 ; FILING DATE: 19-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO US93/02569
 ; FILING DATE: 19-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/126,588
 ; FILING DATE: 24-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 770 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-956-652-12

Query Match 99.6%; Score 1167; DB 3; Length 770;

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Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQMKOQLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQMKOQLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPNICLDRLENWITSLSAQSLOTRQOIKKLEEQKVS YKGDPIVQHRPMLERI 180
Db 250 ACIGGPNICLDRLENWITSLSAQSLOTRQOIKKLEEQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLPVKTGVQFTTKVRLLVKPEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLPVKTGVQFTTKVRLLVKPEL 358

RESULT 10
US-08-956-869-12
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELETYPE: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12

Query Match 99.6%; Score 1167; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQMKOQLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQMKOQLEQMLTALDOMRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPNICLDRLENWITSLSAQSLOTRQOIKKLEEQKVS YKGDPIVQHRPMLERI 180
Db 250 ACIGGPNICLDRLENWITSLSAQSLOTRQOIKKLEEQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLPVKTGVQFTTKVRLLVKPEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLPVKTGVQFTTKVRLLVKPEL 358

RESULT 11
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12

Query Match 99.6%; Score 1167; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQKQKVVENLQDDDFNFKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQKQKVVENLQDDDFNFKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGPPNICLDRLNNITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLNNITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 12
US-09-364-970-3
Sequence 3, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-3

Query Match 99.6%; Score 1167; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQKQKVVENLQDDDFNFKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQKQKVVENLQDDDFNFKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGPPNICLDRLNNITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLNNITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 13
US-09-364-970-5
Sequence 5, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-5

Query Match 99.6%; Score 1167; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQKQKVVENLQDDDFNFKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQQLLEQHAQDVRRVQDLQKQKVVENLQDDDFNFKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQQLLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGPPNICLDRLNNITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGPPNICLDRLNNITSLAESQLQTRQIKKLEIQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 14
US-08-956-653A-12
Sequence 12, Application US/08956653A
Patent No. 6338949
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994

; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-956-653A-12

Query Match 99.6%; Score 1167; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249

QY 121 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPEL 358

RESULT 15
US-08-212-185-12
; Sequence 12, Application US/08212185
; Patent No. 6605442
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James B.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-212-185-12

Query Match 99.6%; Score 1167; DB 4; Length 770;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSGQDMQDLN 189

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Db 190 GNNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249

QY 121 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLENWITSLSAQLOTRQOIKKLEELQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKPEL 358

Search completed: May 25, 2005, 17:47:40
Job time : 29.6534 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:36:58 ; Search time 100.287 Seconds
(without alignments)
763.830 Million cell updates/sec

Title: US-10-090-185-30
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQMLEQHAQ.....IKTGVOFTKRVLLVKFPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1167	99.6	229	13	US-10-090-185-18
3	1167	99.6	229	13	US-10-090-185-28
4	1167	99.6	252	13	US-10-090-185-14
5	1167	99.6	271	13	US-10-090-185-9
6	1167	99.6	770	11	US-09-876-773-12
7	1167	99.6	770	17	US-10-639-617-11
8	1163	99.2	229	13	US-10-090-185-31
9	1156	98.6	720	15	US-10-380-020-4
10	1156	98.6	769	15	US-10-380-020-2
11	1156	98.6	769	15	US-10-380-020-5
12	1156	98.6	770	14	US-10-045-792-8
13	1156	98.6	770	14	US-10-038-010-56

14	1156	98.6	770	14	US-10-117-087-2	Sequence 2, Appli
15	1156	98.6	793	9	US-09-925-302-780	Sequence 780, App
16	1156	98.6	793	10	US-09-925-302-780	Sequence 780, App
17	1153	98.4	770	15	US-10-116-275-329	Sequence 329, App
18	1151	98.2	770	15	US-10-116-275-349	Sequence 349, App
19	1150	98.1	229	13	US-10-090-185-29	Sequence 29, Appl
20	1089	92.9	213	13	US-10-090-185-19	Sequence 19, Appl
21	1089	92.9	236	13	US-10-090-185-15	Sequence 15, Appl
22	1044	89.1	223	13	US-10-090-185-22	Sequence 22, Appl
23	845	72.1	185	13	US-10-090-185-23	Sequence 23, Appl
24	776	66.2	176	13	US-10-090-185-16	Sequence 16, Appl
25	653	55.7	128	13	US-10-090-185-20	Sequence 20, Appl
26	600	51.2	143	13	US-10-090-185-17	Sequence 17, Appl
27	576	49.1	749	9	US-09-833-205-4	Sequence 4, Appli
28	572	48.8	268	13	US-10-090-185-12	Sequence 12, Appl
29	572	48.8	582	14	US-10-245-120-3	Sequence 3, Appli
30	572	48.8	712	11	US-09-876-773-6	Sequence 6, Appli
31	572	48.8	712	14	US-10-245-120-2	Sequence 2, Appli
32	572	48.8	712	17	US-10-639-617-6	Sequence 6, Appli
33	572	48.8	712	17	US-10-936-390-5	Sequence 2, Appli
34	572	48.8	750	9	US-09-833-205-2	Sequence 4, Appli
35	572	48.8	750	11	US-09-876-773-4	Sequence 1, Appli
36	572	48.8	750	14	US-10-245-120-1	Sequence 44, Appl
37	572	48.8	750	14	US-10-308-279-44	Sequence 352, App
38	572	48.8	750	16	US-10-755-889-352	Sequence 823, App
39	572	48.8	750	16	US-10-755-889-823	Sequence 19, Appl
40	572	48.8	750	17	US-10-492-043-19	Sequence 4, Appli
41	572	48.8	750	17	US-10-639-617-4	Sequence 550, App
42	572	48.8	786	9	US-09-925-297-550	Sequence 24, Appl
43	571	48.7	129	13	US-10-090-185-24	Sequence 6, Appli
44	565	48.2	749	9	US-09-833-205-6	Sequence 8, Appli
45	565	48.2	749	11	US-09-876-773-8	

ALIGNMENTS

RESULT 1

US-10-090-185-30
; Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-30

Query Match 100.0%; Score 1172; DB 13; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.3e-95;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	NHPTAAVTEKQMLEQHAQDVQRKRVQDLEQKMKVVENLODDPDPFYKTLKSGQMDQLN	60
Db	1	NHPTAAVTEKQMLEQHAQDVQRKRVQDLEQKMKVVENLODDPDPFYKTLKSGQMDQLN	60
Qy	61	GNNQSVTRKMOQLEQMLTALDQMRRSIVSELAGLISAMEYYQKTLTDBELADWKRREI	120
Db	61	GNNQSVTRKMOQLEQMLTALDQMRRSIVSELAGLISAMEYYQKTLTDBELADWKRREI	120

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Qy 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Db 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
Db 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 2
US-10-090-185-18
; Sequence 18, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzseszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-18

Query Match 99.6%; Score 1167; DB 13; Length 229;
Best Local Similarity 99.6%; Pred. No. 6.4e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
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Db 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Qy 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
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Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
Db 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 3
US-10-090-185-28
; Sequence 28, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzseszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-28

Query Match 99.6%; Score 1167; DB 13; Length 229;
Best Local Similarity 99.6%; Pred. No. 6.4e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
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Qy 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Qy 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Db 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
Db 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 4
US-10-090-185-14
; Sequence 14, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzseszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14

Query Match 99.6%; Score 1167; DB 13; Length 252;
Best Local Similarity 99.6%; Pred. No. 7.2e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Qy 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Qy 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Db 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
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Db 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 5
US-10-090-185-9
; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzseszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-9

Query Match 99.6%; Score 1167; DB 13; Length 229;
Best Local Similarity 99.6%; Pred. No. 6.4e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
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Qy 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Qy 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Db 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
Db 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
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; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-28

Query Match 99.6%; Score 1167; DB 13; Length 229;
Best Local Similarity 99.6%; Pred. No. 6.4e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NHPTAAVVTKEQOMLEQHAQDVVKRVQDLEQKMKVVENLQDDPDFNYKTLKSQGMQDLN 60
Db 1 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDPDFNYKTLKSQGMQDLN 60
Qy 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Qy 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Db 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
Db 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 4
US-10-090-185-14
; Sequence 14, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzseszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14

Query Match 99.6%; Score 1167; DB 13; Length 252;
Best Local Similarity 99.6%; Pred. No. 7.2e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 24 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDPDFNYKTLKSQGMQDLN 83
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Db 84 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
Qy 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Db 144 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 203
Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
Db 204 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 252

RESULT 5
US-10-090-185-9
; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzseszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-9

Query Match 99.6%; Score 1167; DB 13; Length 229;
Best Local Similarity 99.6%; Pred. No. 6.4e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NHPTAAVVTKEQOMLEQHAQDVVKRVQDLEQKMKVVENLQDDPDFNYKTLKSQGMQDLN 60
Db 24 NHPTAAVVTKEQOMLEQHLQDVVKRVQDLEQKMKVVENLQDDPDFNYKTLKSQGMQDLN 83
Qy 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
Db 84 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 143
Qy 121 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 180
Db 144 ACIGPPNICLDRLNWIISLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPMLERI 203
Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
Db 204 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 252
```

; Sequence 9, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzieszczyńska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR P
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-9

Query Match 99.6%; Score 1167; DB 13; Length 271;
Best Local Similarity 99.6%; Pred. No. 7.9e-95;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
Db 24 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 83
QY 61 GNNQSVTRKMOQLEQMLTALDOMRBSIVSELAGLLSAMEYVOKTLTDEELADWKRPEI 120
Db 84 GNNQSVTRKMOQLEQMLTALDOMRBSIVSELAGLLSAMEYVOKTLTDEELADWKRPEI 143
QY 121 ACIGGPPNICLDRLNENWITSLAESQLQTRQIQKLEELQKVKYKGDPIVQHRPMLERI 180
Db 144 ACIGGPPNICLDRLNENWITSLAESQLQTRQIQKLEELQKVKYKGDPIVQHRPMLERI 203
QY 181 VELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKPPPEL 229
Db 204 VELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKPPPEL 252

RESULT 6
US-09-876-773-12
; Sequence 12, Application US/09876773
; Publication No. US20040058318A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,773
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match 99.6%; Score 1167; DB 11; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
Db 130 NHPTAAVTEKQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 189
QY 61 GNNQSVTRKMOQLEQMLTALDOMRBSIVSELAGLLSAMEYVOKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRKMOQLEQMLTALDOMRBSIVSELAGLLSAMEYVOKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNICLDRLNENWITSLAESQLQTRQIQKLEELQKVKYKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLNENWITSLAESQLQTRQIQKLEELQKVKYKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKPPPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKPPPEL 358

RESULT 7
US-10-639-617-12
; Sequence 12, Application US/10639617
; Publication No. US20050079543A1
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; Schindler, Christian W.
; Fu, Xian-Yuan
; Wen, Zilong
; Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/639,617
FILING DATE: 12-AUG-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

Query Match 99.6%; Score 1167; DB 17; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-94; Mismatches 0; Indels 0; Gaps 0;
Matches 228; Conservative 0;
QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLODDDFNFKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLODDDFNFKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
QY 121 ACIGGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 8
US-10-090-185-31
Sequence 31, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
TITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
LENGTH: 229

TYPE: PRT
ORGANISM: Mus musculus
US-10-090-185-31
Query Match 99.2%; Score 1163; DB 13; Length 229;
Best Local Similarity 99.1%; Pred. No. 1.4e-94;
Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLODDDFNFKTLKSGQDMQDLN 60
DB 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLODDDFNFKTLKSGQDMQDLN 60
QY 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
QY 121 ACIGGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 180
DB 121 ACIGGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 180
QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229
DB 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229

RESULT 9
US-10-380-020-4
Sequence 4, Application US/10380020
Publication No. US20040052762A1
GENERAL INFORMATION:
APPLICANT: Yu, Hua
APPLICANT: Pardoll, Drew
APPLICANT: Jove, Richard
APPLICANT: Dalton, William
TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
FILE REFERENCE: 10873-009-999
CURRENT APPLICATION NUMBER: US/10/380,020
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: 60/231,212
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 720
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-380-020-4

Query Match 98.6%; Score 1156; DB 15; Length 720;
Best Local Similarity 98.7%; Pred. No. 2.6e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLODDDFNFKTLKSGQDMQDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLODDDFNFKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKMQQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
QY 121 ACIGGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 180
DB 250 ACIGGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERI 309
QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358
RESULT 10
US-10-380-020-2
Sequence 2, Application US/10380020
Publication No. US20040052762A1

```

; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; PRIOR FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 769
; TYPE: PRT<
; ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match      98.6%; Score 1156; DB 15; Length 769;
Best Local Similarity 98.7%; Pred. No. 2.8e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 NHPTAAVTEKQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB      130 NHPTAAVTEKQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY      61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
DB      190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRQOI 249
QY      121 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLEELQKQVSKGDPVIVQHRPMLERI 180
DB      250 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLEELQKQVSKGDPVIVQHRPMLERI 309
QY      181 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPEL 229
DB      310 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPEL 358

RESULT 11
US-10-380-020-5
; Sequence 5, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-5

Query Match      98.6%; Score 1156; DB 15; Length 769;
Best Local Similarity 98.7%; Pred. No. 2.8e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 NHPTAAVTEKQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB      130 NHPTAAVTEKQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY      61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
DB      190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRQOI 249
QY      121 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLEELQKQVSKGDPVIVQHRPMLERI 180
DB      250 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLEELQKQVSKGDPVIVQHRPMLERI 309
QY      181 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPEL 229
DB      310 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPEL 358

; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; CURRENT FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match      98.6%; Score 1156; DB 15; Length 769;
Best Local Similarity 98.7%; Pred. No. 2.8e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 NHPTAAVTEKQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB      130 NHPTAAVTEKQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY      61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
DB      190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRQOI 249
QY      121 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLEELQKQVSKGDPVIVQHRPMLERI 180
DB      250 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLEELQKQVSKGDPVIVQHRPMLERI 309
QY      181 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPEL 229
DB      310 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPEL 358
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DB      190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRQOI 249
QY      121 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLEELQKQVSKGDPVIVQHRPMLERI 180
DB      250 ACIGGPNICLDRLENWITSLAESQLQTRQIQKLEELQKQVSKGDPVIVQHRPMLERI 309
QY      181 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPEL 229
DB      310 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPEL 358

RESULT 12
US-10-045-792-8
; Sequence 8, Application US/10045792
; Publication No. US20030003563A1
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/045,792
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8

Query Match      98.6%; Score 1156; DB 14; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.9e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 NHPTAAVTEKQOMLEQHAQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
DB      130 NHPTAAVTEKQOMLEQHLQDVRRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY      61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRPEI 120
DB      190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRQOI 249
```

QY 121 ACIGPPNICLDRLNWTSLAESQLTROQIKKLELOKQSVYKGDPIVQHRPMLERI 180
 Db 250 ACIGPPNICLDRLNWTSLAESQLTROQIKKLELOKQSVYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 358

RESULT 13

US-10-038-010-56
 ; Sequence 56, Application US/10038010
 ; Publication No. US20030040089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HYBRIGENICS
 ; APPLICANT: Pierre, Legrain
 ; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
 ; FILE REFERENCE: B4767A
 ; CURRENT APPLICATION NUMBER: US/10/038,010
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US 60/259,377
 ; PRIOR FILING DATE: 2001-01-02
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 56
 ; LENGTH: 770
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: STAT3 : Transcription factor
 ; LOCATION: (1)..(770)
 ; OTHER INFORMATION:
 ; OTHER INFORMATION:
 ; OTHER INFORMATION:

Query Match 98.6%; Score 1156; DB 14; Length 770;
 Best Local Similarity 98.7%; Pred. No. 2.9e-93;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLODDDFNFKYTKLSQGDMDLN 60
 Db 130 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLODDDFNFKYTKLSQGDMDLN 189
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
 QY 121 ACIGPPNICLDRLNWTSLAESQLTROQIKKLELOKQSVYKGDPIVQHRPMLERI 180
 Db 250 ACIGPPNICLDRLNWTSLAESQLTROQIKKLELOKQSVYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 358

RESULT 14

US-10-117-087-2
 ; Sequence 2, Application US/10117087
 ; Publication No. US20030166854A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SERLUP-CRESCENZI, Ottaviano
 ; APPLICANT: DELLA PIETRA, Linda
 ; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
 ; FILE REFERENCE: SERLUP-2
 ; CURRENT APPLICATION NUMBER: US/10/117,087
 ; CURRENT FILING DATE: 2002-04-08
 ; PRIOR APPLICATION NUMBER: US/09/526,542
 ; PRIOR FILING DATE: 2000-03-19
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 770
 ; TYPE: PRT

; ORGANISM: Human
 US-10-117-087-2
 Query Match 98.6%; Score 1156; DB 14; Length 770;
 Best Local Similarity 98.7%; Pred. No. 2.9e-93;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLODDDFNFKYTKLSQGDMDLN 60
 Db 130 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLODDDFNFKYTKLSQGDMDLN 189
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
 QY 121 ACIGPPNICLDRLNWTSLAESQLTROQIKKLELOKQSVYKGDPIVQHRPMLERI 180
 Db 250 ACIGPPNICLDRLNWTSLAESQLTROQIKKLELOKQSVYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 358

RESULT 15

US-09-925-302-780
 ; Sequence 780, Application US/09925302
 ; Patent No. US20020044941A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA104
 ; CURRENT APPLICATION NUMBER: US/09/925,302
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05918
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 896
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 780
 ; LENGTH: 793
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 US-09-925-302-780

Query Match 98.6%; Score 1156; DB 9; Length 793;
 Best Local Similarity 98.7%; Pred. No. 3e-93;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLODDDFNFKYTKLSQGDMDLN 60
 Db 153 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLODDDFNFKYTKLSQGDMDLN 212
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
 Db 213 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 272
 QY 121 ACIGPPNICLDRLNWTSLAESQLTROQIKKLELOKQSVYKGDPIVQHRPMLERI 180
 Db 273 ACIGPPNICLDRLNWTSLAESQLTROQIKKLELOKQSVYKGDPIVQHRPMLERI 332
 QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 229
 Db 333 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPPPEL 381

Search completed: May 25, 2005, 18:21:54
 Job time : 101.62 secs

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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:24:07 ; Search time 21.6038 Seconds
(without alignments)
1019.898 Million cell updates/sec

Title: US-10-090-185-30
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQOMLEQHAQ.....IKTGVOFTTKVRLLVKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1156	98.6	770	2 I49508	ISGF3 p91-related
2	1151	98.2	770	2 A54444	DNA-binding protei
3	526.5	44.9	739	2 A46159	interferon-depende
4	511	43.6	748	2 A56047	gamma-interferon a
5	321	27.4	851	2 A46160	interferon alpha-1
6	268.5	22.9	786	2 I49274	mammary gland fact
7	268.5	22.9	793	2 S54772	mammary gland fact
8	262.5	22.4	794	2 G02317	transcription acti
9	237	20.2	794	2 S55527	mammary gland fact
10	124.5	10.6	848	2 A54740	interleukin-4 indu
11	121	10.3	978	2 A70387	conserved hypothet
12	119.5	10.2	837	2 I57557	DNA-Binding Protei
13	119.5	10.2	2094	2 S33124	tpi protein - huma
14	119	10.2	533	2 G72593	hypothetical prote
15	118.5	10.1	1166	2 T27075	hypothetical prote
16	118.5	10.1	1208	2 AE1947	chromosome segrega
17	116	9.9	1164	2 T24806	hypothetical prote
18	115	9.8	289	2 S51193	epimorphin - mouse
19	113.5	9.7	1690	2 T13030	microtubule bindin
20	113	9.6	1976	2 A59252	myosin heavy chain
21	113	9.6	1999	1 S21801	myosin heavy chain
22	113	9.6	3187	2 JCS937	364K Golgi complex
23	112.5	9.6	1957	2 T38077	hypothetical coile
24	112	9.6	3685	1 A27605	dystrophin, muscle
25	111.5	9.5	747	1 A57107	kinesin-related pr
26	111.5	9.5	750	2 T38435	coiled coil protei
27	111.5	9.5	857	2 S33821	median body protei
28	111.5	9.5	1178	2 S30431	MSP-300 protein -
29	110.5	9.4	896	2 S43074	epidermal growth f

30	110.5	9.4	924	2 S06117	myosin heavy chain
31	110	9.4	1959	1 A33977	myosin heavy chain
32	109.5	9.3	1992	2 A47297	myosin heavy chain
33	109.5	9.3	2007	1 B43402	myosin heavy chain
34	108.5	9.3	727	2 AC1814	hypothetical prote
35	108.5	9.3	1972	1 A41604	myosin heavy chain
36	108	9.2	464	2 H90279	microtubule bindin
37	108	9.2	734	2 T27055	hypothetical prote
38	108	9.2	1269	2 F84730	probable myosin he
39	107.5	9.2	946	2 S28061	SCP1 protein - rat
40	107.5	9.2	1008	2 AE2304	hypothetical prote
41	107.5	9.2	1509	1 A27224	myosin heavy chain
42	107.5	9.2	1940	2 A59287	myosin heavy chain
43	107.5	9.2	1963	1 MWKW	myosin heavy chain
44	107.5	9.2	2253	2 T30336	nuclear/mitotic ap
45	107	9.1	564	2 A60115	M protein precursor

ALIGNMENTS

RESULT 1

I49508
ISGF3 p91-related transcription factor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49508; I49009
R;Akita, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, K.; Yoshida, K.; Su
Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr
A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: I49508
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P42227; GB:L29278; NID:g476715; PIDN:AAA37254.1; PID:g47671
R;Raz, R.; Durbin, J.E.; Levy, D.E.
J. Biol. Chem. 269, 24391-24395, 1994
A;Title: Acute phase response factor and additional members of the interferon-stimulate
A;Reference number: I49009; MUID:95014185; PMID:7523373
A;Accession: I49009
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-393,'M',395-700,702-770 <RE2>
A;Cross-references: EMBL:U08378; NID:g473889; PIDN:AAA56668.1; PID:g473890
C;Genetics:
A;Gene: APRF
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match	98.6%	Score	1156	DB	2	Length	770
Best Local Similarity	98.7%	Pred. No.	1.8e-69				
Mismatches	226	Conservative	1	Mismatches	2	Indels	0
Gaps	0						
QY	1	NHPTAAVTEKQOMLEQHAQDVVKRVQDLLEQKMKVVENLODDDFNYKTLKSGQMDLNL	60				
DB	130	NHPTAAVTEKQOMLEQHLQDVVKRVQDLLEQKMKVVENLODDDFNYKTLKSGQMDLNL	189				
QY	61	GNQSVTRQMKQOQLTALDQMRISIVSELAGLLSAMEYVOKLTLDDELADWKRRPEI	120				
DB	190	GNQSVTRQMKQOQLTALDQMRISIVSELAGLLSAMEYVOKLTLDDELADWKRRQOI	249				
QY	121	ACIGGPPNICLDRLENWITSLAESQLQTRQIKKLELOQKVSFKGDPVVOHRPMLERI	180				
DB	250	ACIGGPPNICLDRLENWITSLAESQLQTRQIKKLELOQKVSFKGDPVVOHRPMLERI	309				
QY	181	VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL	229				
DB	310	VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL	358				

RESULT 2
A54444
DNA-binding protein APRF - human

C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: A54444
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud
Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRE, a novel IFN-stimulated gene factor 3 p91-related tra
A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: A54444
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789
C;Genetics:
A;Gene: GDB:STAT3; APRE
A;Cross-references: GDB:358950
A;Map position: 17q21-17q21
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor

Query Match 98.2%; Score 1151; DB 2; Length 770;
Best Local Similarity 98.3%; Pred. No. 4e-69;
Matches 225; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NHPTAAVTEKQMLEQHAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVTEKQMLEQHLQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189

Qy 61 GNNQSVTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKTLTDEELADWKRQOI 249

Qy 121 ACIGGPNICLDRLNWTSLAESQLQTRQIKKLELQKVSYKGDPIVQHRPMLERI 180
Db 250 ACIGGPNICLDRLNWTSLAESQLQTRQIKKLELQKVSYKGDPIVQHRPMLERI 309

Qy 181 VELFRNLKMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 358

RESULT 3
A46159
interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Improt, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91- and 84-kDa ISG
A;Reference number: A46159; MUID:92366557; PMID:1502203
A;Accession: A46159
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
A;Cross-references: UNIPROT:P42224
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 44.9%; Score 526.5; DB 2; Length 739;
Best Local Similarity 46.2%; Pred. No. 1.3e-27;
Matches 104; Conservative 48; Mismatches 60; Indels 13; Gaps 2;

Qy 5 AAVTEKQMLEQHAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 64
Db 132 STVMLDKQKELDSKVRKVKVCMIEHIEIKSLDQYDFKCKTL--QNRHETNGVAK 189

Qy 65 SVTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKTLTDEELADWKRPEIACIG 124
Db 190 SDQKQEQLLKXVLMNDKKEVVKHIIELNVTETQALINDELVEWKRQOOSACIG 249

Qy 125 GPPNICLDRLNWTSLAESQLQTRQIKKLELQKVSYKGDPIVQHRPMLERI 184
Db 310 GPPNICLDRLNWTSLAESQLQTRQIKKLELQKVSYKGDPIVQHRPMLERI 358

Db 250 GPPNACLDQLQ-----QVRQQLKLELEQKYVEHDPITKNQKQVLDWRTFSLF 298

Qy 185 RNLKMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 229
Db 299 QQLIQSFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 343

RESULT 4
A56047
gamma-interferon activation site-binding protein Stat4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins
Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in e
A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-748 <YAM>
A;Cross-references: UNIPROT:P42228; GB:U09351; NID:g509502; PID:AAA19692.1; PID:g50950
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein

Query Match 43.6%; Score 511; DB 2; Length 748;
Best Local Similarity 45.5%; Pred. No. 1.4e-26;
Matches 102; Conservative 48; Mismatches 66; Indels 8; Gaps 2;

Qy 8 VTEKQMLEQHAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 65
Db 136 VSEQRNVEHKVSAIKNSVQMTQDPTKYLEDLQDFDYRYKTIQTMDQGD-----KNSI 189

Qy 66 VTRQKQMLEQMLTALDQWRRSIVSELAGLLSMEYVQKTLTDEELADWKRPEIACIG 125
Db 190 LVNQEVLTQEMLSLDFKREKLSKMTQIVNETDLMNMSLLEELQDWKKRQOIACIG 249

Qy 126 PPNICLDRLNWTSLAESQLQTRQIKKLELQKVSYKGDPIVQHRPMLERI 185
Db 250 PLHNGLDQQLQNCFTLLAESLFLQRLQLEKLOEQSTKWTVEGDPFPAQRAHLLEATFLIY 309

Qy 186 NLKMSAFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 229
Db 310 NLFKNSFVVERQPCMPHDPRLVTKTGQVFTTKVRLLVKFPPEL 353

RESULT 5
A46160
interferon alpha-induced transcription activator ISGF-3, 113K chain - human
N;Alternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
R;Fu, X.Y.; Schindler, C.; Improt, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator
A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-851 <FU1>
A;Cross-references: UNIPROT:P52630
A;Note: sequence extracted from NCBI backbone (NCBIP:110820)
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell, J.E.
submitted to the EMBL Data Library, December 1994
A;Reference number: S71908
A;Accession: S71908
A;Molecule type: DNA
A;Residues: 1-851 <YAN>
A;Cross-references: EMBL:U18671; NID:g1293919; PID:AAA98760.1; PID:g1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in

A:Reference number: S53873; MUID:95192056; PMID:7885841

A:Accession: S53873

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-196;392-591;684-730 <YAW>

A:Cross-references: EMBL:U18671

A:Genetics:

A:Gene: stat2

A:Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 365/2; 372/2; 40

C:Superfamily: human signal transducer and transcription activator STAT5A

C:Keywords: signal transduction; transcription regulation

Query Match 27.4%; Score 321; DB 2; Length 851;

Best Local Similarity 33.5%; Pred. No. 7e-14;

Matches 74; Conservative 51; Mismatches 90; Indels 6; Gaps 4;

QY 8 VTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFYKTLKSGQMDLNGNNSVT 67

DB 138 VSSQHEISRIIDLAMMEKLKVSISQLKDDQDVECFRYK-IOAKGKTPSLDPH--QTK 194

QY 68 ROKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDELDWKRRPEIACIGGPP 127

DB 195 EQKI--LQETNELDKRRKREVDLASKALLGRLTTLIELLL-PKLEBKAQQQKACIRAPI 251

QY 128 NCLDLRENWITSLASSQIQTRQIKKLELOKQVSGDPIVOHRPMLERIVELFRNL 187

DB 252 DHGLEQLEWTFAGAKLLFHLRLKELKSLGSLVSYQDDPLTKGVDLRLNAQVTELLQRL 311

QY 188 MKSAFVVERQPCMPHDPRLVKTGVQVTTKVRLLAVKPE 228

DB 312 LHRFAVVEVTPCQMPQTPHRLILKTKSGKFTVTRLRLVQ 352

RESULT 6

I49274

mammary gland factor - mouse

N:Alternate names: STAT5 protein homolog p80

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49274; S54773; S54727

R:Liou, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A:Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved in

A:Reference number: I49273; MUID:96004632; PMID:7568026

A:Accession: I49274

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-786 <RES>

A:Cross-references: UNIPROT:P42232; UNIPROT:Q9JUM1; EMBL:U21110; NID:g747973; PIDN:AA052

R:Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A:Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A:Reference number: S54772; MUID:95237198; PMID:7720707

A:Accession: S54773

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-432, 'E', 434-786 <MUI>

A:Cross-references: EMBL:Z48539; NID:g758635; PIDN:CAA88420.1; PID:g758636

R:Azam, M.; Erdjument-Bromage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,

EMBO J. 14, 1402-1411, 1995

A:Title: Interleukin-3 signals through multiple isoforms of Stat5.

A:Reference number: S54725; MUID:95246733; PMID:7537213

A:Accession: S54727

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-432, 'E', 434-786 <AZA>

C:Genetics:

A:Gene: Stat5b

C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.9%; Score 268.5; DB 2; Length 786;

Best Local Similarity 30.6%; Pred. No. 2e-10;

Matches 71; Conservative 42; Mismatches 98; Indels 21; Gaps 5;

RESULT 8

G02317

transcription activator stat5a - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text_change 09-Jul-2004

QY 5 AAVVTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFY-KTLKSGQMDLNGNN 63

DB 134 ADAMSQKHLQINQTFEELRLITQDTENELKLCQQTOEYFIIOQESLRIOAQFAQLGQLN 193

QY 64 -----QSVTRQKMQQLEQML-----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELA 112

DB 194 PORMSRRETALQCKQVSLQVLEWQRAQTLQQRVLAERKQKTLQLLRQKQTLIDDELI 253

QY 113 DWKRPEIACIGPPNICLDRLNENWITSLAESQLQTRQIKKLEELQKQVSGDPIVQHV 172

DB 254 QMKRRQQLAGNGGPPGSLDLVLSWCEKLAELIWNQRIIRRAEHLCCQLPIPG-PVEEM 312

QY 173 RPLMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQVTTKVRLLV 224

DB 313 LAENVATITDIISALVTSTFIIEKQP-----PQVLKATQTKFAATVRLLV 356

RESULT 7

S54772

mammary gland factor - mouse

N:Alternate names: stat5 protein

C:Species: Mus musculus (house mouse)

C:Date: 27-Oct-1995 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S54772; I49273

R:Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A:Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A:Reference number: S54772; MUID:95237198; PMID:7720707

A:Accession: S54772

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-793 <MUI>

A:Cross-references: UNIPROT:P42230; UNIPROT:Q9JIA0; EMBL:Z48538; NID:g758633; PIDN:CAA8

R:Liou, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A:Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved

A:Reference number: I49273; MUID:96004632; PMID:7568026

A:Accession: I49273

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-793 <RES>

A:Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972

C:Genetics:

A:Gene: Stat5a

C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.9%; Score 268.5; DB 2; Length 793;

Best Local Similarity 30.6%; Pred. No. 2e-10;

Matches 70; Conservative 42; Mismatches 96; Indels 21; Gaps 5;

QY 8 VTEKQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDDFNFY-KTLKSGQMDLNGNN--- 63

DB 137 MSQKHLQINQRFEBULRLITQDTENELKLCQQTOEYFIIOQESLRIOAQFAQLGQLN 196

QY 64 -----QSVTRQKMQQLEQML-----TALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWK 115

DB 197 RMSRETALQCKQVSLQVLEWQRAQTLQQRVLAERKQKTLQLLRQKQTLIDDELIQWK 256

QY 116 RPETACIGPPNICLDRLNENWITSLAESQLQTRQIKKLEELQKQVSGDPIVQHRPM 175

DB 257 RRQQLAGNGGPPGSLDLVLSWCEKLAELIWNQRIIRRAEHLCCQLPIPG-PVEEMLA 315

QY 176 LEERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQVTTKVRLLV 224

DB 316 VNATITDIISALVTSTFIIEKQP-----PQVLKATQTKFAATVRLLV 356

C;Accession: G02317
R;Lin, J.
Submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:gl151169; PID:gl151169
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.4%; Score 262.5; DB 2; Length 794;
Best Local Similarity 30.1%; Pred. No. 5.1e-10;
Matches 69; Conservative 43; Mismatches 96; Indels 21; Gaps 5;

QY 8 VTEKQQLQHAQDVRRKVDLEQKMKVENVLQDDDFNY-KTLKSGQMDL----- 59
DB 137 MSQKHLQINQTFEELRVLTQDTELKLLQOTQBYFIQOESLRIQQAQIAQLNPQE 196
QY 60 NGNNQSVTRQWQQLQML-----TALQMRRSIVSELAGLSAMEYVQKTLTDEELADWK 115
DB 197 RLSHETALQKQVSLQVLEAWLQREAGTLLQYRVLEAEKHQKTLQLLRKQOTIILDELLQWK 256
QY 116 RRPFIACGGPNICLDRLENWITSLSAQLOTRQOIKKLEELQKQVSYKGDPIVQHRPM 175
DB 257 RRQQLAGNGGPPGSLDVLQSWCEKLAETIWNQRRQIRRAEHLCCQQLPIFG-PVEEMLAE 315
QY 176 LEEBIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLV 224
DB 316 VNATITDIISALVTSFIIEKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 9
S55527
mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55527; S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regulat
A;Reference number: S55527; MUID:95188889; PMID:7882987
A;Accession: S55527
A;Molecule type: mRNA
A;Residues: 1-794 <WAK>
A;Cross-references: UNIPROT:P42231; EMBL:X78428; NID:g602354; PIDN:CAA55191.1; PID:g6023
A;Note: this is a revision to the sequence from reference S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 13, 2182-2191, 1994
A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcri
A;Reference number: S44353; MUID:94244619; PMID:7514531
A;Accession: S44353
A;Molecule type: mRNA
A;Residues: 1-716; 'RHLHGSGLSR', 729, 'P', 731, 'ASL' <WAW>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S55527
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 20.2%; Score 237; DB 2; Length 794;
Best Local Similarity 29.3%; Pred. No. 2.5e-08;
Matches 67; Conservative 42; Mismatches 98; Indels 22; Gaps 6;

QY 8 VTEKQQLQHAQDVRRKVDLEQKMKVENVLQDDDFNY-KTLKSGQMDLNGNN--- 63
DB 138 MSQKHLQINQTFEELRVLTQDTELKLLQOTQBYFIQOESLRIQQAQIAQLNPQE 197
QY 64 ----QSVTRQWQQLQML-----TALQMRRSIVSELAGLSAMEYVQKTLTDEELADWK 115
DB 198 RLSHETALQKQVSLQVLEAWLQREAGTLLQYRVLEAEKHQKTLQLLRKQOTIILDELLQWK 257
QY 116 RRPFIACGGPNICLDRLENWITSLSAQLOTRQOIKKLEELQKQVSYKGDPIVQHRPM 175
DB 258 RRHWRGMEAPPR-SLDVLQSWCEKLAETIWNQRRQIRRAEHLCCQQLPIFG-PVEEMLAE 315

QY 176 LEEBIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLVV 224
DB 316 VNATITDIISALVTSFIIEKQP-----PQVLKTQTKFAATVRLVV 356

RESULT 10
A54740
interleukin-4-induced transcription factor stat - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
R;Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID:94367369; PMID:8085155
A;Accession: A54740
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-848 <HOU>
A;Cross-references: UNIPROT:P42226
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription regulation

Query Match 10.6%; Score 124.5; DB 2; Length 848;
Best Local Similarity 29.7%; Pred. No. 0.82;
Matches 41; Conservative 22; Mismatches 52; Indels 23; Gaps 4;

QY 88 IVSELAGLSAMEYVQKTLTDEELADWKRPETACTGGPNICLDRLENWITSLSAQLO 147
DB 182 LLOFTTGELEA---AKALVLKRIQIWKRRQQQLAGNGAP-----FEESLAPLQER 227
QY 148 TRQIKKLEELQKQVSYKGDPI-VOHRPMLLEBRIVELFRNLKMSAFVVERQPCMPHDPDR 206
DB 228 CESLVDIYSQLQOEVGAGGELEPKTRASLTGRLDEVLRITVTSCLFVEKQP----- 279
QY 207 PLVIKTGVQFTTKVRLVV 224
DB 280 PQVLKTQTKFQAGVRELL 297

RESULT 11
A70387
conserved hypothetical protein aq_1006 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A70387
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: A70387
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-978 <AQF>
A;Cross-references: UNIPROT:O67124; GB:AE000718; NID:g2983504; PIDN:AAC07092.1; PID:g29
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_1006
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match 10.3%; Score 121; DB 2; Length 978;
Best Local Similarity 23.3%; Pred. No. 1.7;
Matches 49; Conservative 38; Mismatches 81; Indels 42; Gaps 6;

QY 10 EKOQMLEQHAQDVRRKVDLEQKMKVENVLQDDDFNYKTLKSGQMDLNGNNQSVTRQ 69
DB 234 EEDSLERELSQQVTKLELENKEVEKLEKLEFSRKVAP-----YVPIAK 281
QY 70 KMQQLQFMTALQMRRSIVSELAGLSAMEYVQKTLT-----DEELAD- 113
DB 282 RIBEIDKDLTELKVRKNKTKLAVLKDLSLFAQEEELNRIEAEKFKPEKEKELEHR 341

A:Molecule type: mRNA
A:Residues: 1-725,'L' <MI2>
A:Cross-references: EMBL:X63105; NID:g37257; PIDN:CAA44819.1; PID:g37258
R:King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.
Oncogene 2, 617-619, 1988
A:Title: Top homologues activate met and raf
A:Reference number: S00928; MUID:88262257; PMID:3387099
A:Accession: S00928
A:Molecule type: mRNA
A:Residues: 1-31,'R',33-142 <KIN>
A:Cross-references: EMBL:Y00672; NID:g37255; PIDN:CAA68681.1; PID:g37256
R:Greco, A.
submitted to the EMBL Data Library, December 1995
A:Reference number: H00592
A:Accession: G01185
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 144-228 <GRE>
A:Cross-references: EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; PID:g1296798
C:Genetics:
A:Gene: GDB:TPR
A:Cross-references: GDB:I28821; OMIM:189940
A:Map position: lq25-lq25
A:Introns: 177/3

Query Match 10.2%; Score 119.5; DB 2; Length 2094;
Best Local Similarity 20.4%; Pred. No. 5.1;
Matches 45; Conservative 50; Mismatches 81; Indels 45; Gaps 6;

Qy 6 AVTTEQOMLEQHAQVVRK-----RVODLEQKMKV---VENLQDDFFNYK 48
Db 1387 ASLTNNQNLQSLKEDLNKVRTEKETIQKDLDAKIIDIOEKVKTIQVKKIGRRYKTOYE 1446
Qy 49 TLKSO-----GMDQLNGNQSVTRKMOQLSOMLTALDQMRSSIVSELGLL 96
Db 1447 ELKAOQDKVMTSAQSSGDHQE-----QHVSVQEMQELKETTQAKTSKSLESQ----- 1496
Qy 97 SAMEYVQKTLTDELDADWKKRPEIACIGGPPNICLDRLNWIITSLAESLOLRQKIKCLE 156
Db 1497 --VENLQKTLSEKETEARNLQEQTVQLQSE---LSLRQDLQDRTTQBEQLRQKITEKE 1550
Qy 157 ELQOKYSYKGDPIVQHRPMLERIVELFRNLKSAFVVRQ 197
Db 1551 EKTRKAIVAASKIAHLAGYKQDLTKENBELKORNGALDQ 1591

RESULT 14

Hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: G72593
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, M.;
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon.
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72593
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-533 <RAW>
A:Cross-references: UNIPROT:Q9YCP2; DDBJ:AF000061; NID:G5104821; PIDN:BAAB80205.1
C:Genetics:
A:Gene: APE1216

Query Match 10.2%; Score 119; DB 2; Length 533;
Best Local Similarity 20.7%; Pred. No. 1.1;
Matches 41; Conservative 49; Mismatches 66; Indels 42; Gaps 7;

Qy 8 VTEQOMLEQHAQVVRKRVODLEQKMKVVEN-----LQDDF-----DFNYK 48
Db 319 MSQOLAAEDLFSLSRVVEDLEARYGSVEDRLSQAEEDISLTSLDSLRTELEDLSTR 378

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:15:30 ; Search time 95.284 Seconds
(without alignments)
1230.701 Million cell updates/sec

Title: US-10-090-185-30

Perfect score: 1172
Sequence: 1 NHPTRAVTEKQOMLEQHAQ.....IKTGVOFTTKVRLLYKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Length	DB ID	Description
1	1156	98.6	770	1	STA3 HUMAN	P40763 homo sapien
2	1156	98.6	770	1	STA3 MOUSE	P42227 mus musculus
3	1153	98.4	770	1	STA3 RAT	P52631 rattus norv
4	1149	98.0	770	1	STA3 BOVIN	P61635 bos taurus
5	1131	96.5	771	2	O6DV79	O6dv79 gallus gall
6	1098	93.7	769	2	Q9PVX8	Q9pvx8 xenopus lae
7	1095	93.4	766	2	Q7ZXK3	Q7zxk3 xenopus lae
8	1010	86.2	414	2	Q7ZTS5	Q7zts5 brachydanio
9	1010	86.2	765	2	O6DVF3	O6dvf3 oryzias lat
10	1010	86.2	785	2	O6GUE7	O6gue7 oryzias lat
11	1010	86.2	786	2	O6NV46	O6nv46 brachydanio
12	1010	86.2	806	2	O93599	O93599 brachydanio
13	986	84.1	764	2	O90Y16	O90y16 tetraodon f
14	976	83.3	767	2	O13133	O13133 oncorhynch
15	656	56.0	163	2	O9N145	O9n145 macaca mula
16	578	49.3	751	2	O8JGN0	O8jgn0 xenopus lae
17	576	49.1	712	2	O6PEQ7	O6peq7 rattus norv
18	576	49.1	749	2	O9QXK0	O9qxk0 rattus norv
19	574	49.0	749	2	O8CA97	O8ca97 mus musculus
20	573	48.9	712	2	O99K94	O99k94 mus musculus
21	573	48.9	749	2	O8C3V4	O8c3v4 mus musculus
22	573	48.9	749	2	O9D323	O9d323 mus musculus
23	573	48.9	755	2	O8C8M3	O8c8m3 mus musculus
24	572	48.8	750	1	STA1 HUMAN	P42224 homo sapien
25	572	48.8	750	2	O68D00	O68d00 homo sapien
26	572	48.8	757	2	Q764M5	Q764m5 mus scrofa
27	565	48.2	749	1	STA1 MOUSE	P42225 mus musculus
28	541.5	46.2	754	2	O13131	O13131 oncorhynch
29	535	45.6	749	2	O93598	O93598 brachydanio
30	535	45.6	749	2	Q6P943	Q6p943 brachydanio
31	534	45.6	528	2	O8JFU8	O8jfu8 brachydanio

32	532.5	45.4	108	2	Q704W6	Q704w6 bos taurus
33	530.5	45.3	718	2	Q801Y2	Q801y2 carassius a
34	523	44.6	748	1	STA4 HUMAN	O14765 homo sapien
35	520.5	44.4	758	2	Q90Y17	Q90y17 tetraodon f
36	518.5	44.2	754	2	O13132	O13132 oncorhynch
37	516	44.0	657	2	O8AW24	O8aw24 brachydanio
38	507.5	43.3	749	1	STA4 MOUSE	P42228 mus musculus
39	507	43.3	651	2	Q7Z253	Q7z253 brachydanio
40	507	43.3	667	2	O8AW20	O8aw20 brachydanio
41	506.5	43.2	652	2	Q7Z277	Q7z277 brachydanio
42	506	43.2	553	2	O8JFU7	O8jfu7 brachydanio
43	506	43.2	748	2	O6GHB2	O6ghb2 rattus norv
44	504	43.0	1153	2	Q8JFS5	Q8jfs5 brachydanio
45	494	42.2	737	2	Q90Y15	Q90y15 tetraodon f

ALIGNMENTS

RESULT 1
STA3 HUMAN
ID STA3 HUMAN STANDARD; PRT; 770 AA.
AC P40763; O14916; Q9BW54;
DT 01-FEB-1995 (Rel. 31, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
DE response factor).
GN Name=STAT3; Synonyms=APRF;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;
RA Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.,
RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
RT related transcription factor involved in the gp130-mediated signaling
RT pathway.";
RL Cell 77:63-71(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
RA Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.,
RT "Highly conserved amino-acid sequence between murine STAT3 and a
RL Gene 213:119-124(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattleSeqFe. NHLBI HL66682 program for genomic applications, UW-
RL FHCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
RN [4]
RP Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).
RC TISSUE=Kidney, and Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 564-704 FROM N.A.
 RC TISSUE=Liver;
 RL Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.,
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP PHOSPHORYLATION ON SERINE.
 RX MEDLINE=95215843; PubMed=7701321;
 RA Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.,
 RT "Requirement of serine phosphorylation for formation of STAT-promoter
 RT complexes";
 RL Science 267:1990-1994 (1995).
 RN [7]
 RP INTERACTION WITH NCOAL.
 RX PubMed=1173079; DOI=10.1074/jbc.M11486200;
 RA Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.,
 RT "Functional interaction of STAT3 transcription factor with the
 RT coactivator NcoA/SRC1a";
 RL J. Biol. Chem. 277:8004-8011(2002).
 CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes.
 CC -1- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P40763-1; Sequence=VSP_010474;
 CC Name=Del-701;
 CC IsoId=P40763-2; Sequence=VSP_010474;
 CC TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
 CC muscle, kidney and pancreas.
 CC -1- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, INF-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity.
 CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; L29277; AAA58374.1; -
 CC EMBL; AJ012463; CAAL10032.1; -
 CC EMBL; AY572796; AAS66986.1; -
 CC EMBL; BC000627; AAH00627.1; -
 CC EMBL; BC014482; AAH14482.1; -
 CC EMBL; AF029311; AAB84254.1; -
 CC PIR; A54444; A54444.
 CC HSPSP; P42227; 18G1.
 CC TRANSFAC; T01493; -
 CC Genew; HGNC:11364; STAT3.
 CC H-InvDB; HIX0013840; -
 CC MIM; 102582; -
 CC GO; GO:0005737; C:cytoplasm; TAS.
 CC GO; GO:0005634; C:nucleus; TAS.
 CC GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. .; TAS.

DR GO; GO:0003700; F:transcription factor activity; TAS.
 DR GO; GO:0006928; P:cell motility; TAS.
 DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
 DR GO; GO:0000122; P:negative regulation of transcription from P. .; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR008967; P53 like_DNA_bnd.
 DR InterPro; IPR000980; SH2-
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR PROSITE; PS50001; SH2; 1.
 KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
 KW Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
 FT DOMAIN 580 670 SH2.
 FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 FT MOD_RES 727 727 Phosphoserine (By similarity).
 FT VARSPLIC 701 701 Missing (in isoform Del-701).
 FT FTID=VSP_010474.
 FT VARIANT 32 32 O -> K (in dbSNP:1803125).
 FT FTID=VAR_018683.
 FT VARIANT 143 143 M -> L.
 FT CONFLICT 288 288 Q -> H (in Ref. 1).
 FT CONFLICT 460 460 P -> S (in Ref. 1).
 FT CONFLICT 548 548 K -> N (in Ref. 1).
 FT CONFLICT 561 561 F -> Y (in Ref. 1).
 FT CONFLICT 667 667 V -> L (in Ref. 1).
 FT CONFLICT 730 730 T -> A (in Ref. 1).
 SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;
 Query Match 98.6%; Score 1156; DB 1; Length 770;
 Best Local Similarity 98.7%; Pred. No. 3.1e-05;
 Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVTEKQOMLEQHAQDVVKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
 DB 130 NHPTAAVTEKQOMLEQHLQDVVKRVQDLQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
 QY 61 GNNQSVTRQMQOQLQEMLTALDQMRSSIVSELQGLLSAMEYVQKTLTDESLADKKRPEI 120
 DB 190 GNNQSVTRQMQOQLQEMLTALDQMRSSIVSELQGLLSAMEYVQKTLTDESLADKKRQOI 249
 QY 121 ACTGGPPNICLDLENWITSLAESQLQTRQOIKKLELOQKVKYKGDPIVQHRPMLERI 180
 DB 250 ACTGGPPNICLDLENWITSLAESQLQTRQOIKKLELOQKVKYKGDPIVQHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPEL 229
 DB 310 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPEL 358
 RESULT 2
 STA3 MOUSE
 ID STA3 MOUSE STANDARD; PRT; 770 AA.
 AC P42227;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Signal transducer and activator of transcription 3 (Acute-phase
 DE response factor).
 GN Name=Stat3; Synonyms=Aprf;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
 RP AND 632-640.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;

RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
RT related transcription factor involved in the gp130-mediated signaling
RT pathway.";
RN Cell 77:63-71(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC TISSUE=Thymus;
RX MEDLINE=94118718; PubMed=8140422;
RA Zhong Z., Wen Z., Darnell J.E. Jr.;
RT "Stat3: a STAT family member activated by tyrosine phosphorylation in
RT response to epidermal growth factor and interleukin-6.";
RN Science 264:95-98(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC TISSUE=Brain;
RX MEDLINE=95014185; PubMed=7523373;
RA Raz R., Durbin J.E., Levy D.E.;
RT "Acute phase response factor and additional members of the interferon-
RT stimulated gene factor 3 family integrate diverse signals from
RT cytokines, interferons, and growth factors.";
RN J. Biol. Chem. 269:24391-24395(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM STAT3B).
RC STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
RX MEDLINE=96016116; PubMed=7568080;
RA Schaefer T.S., Sanders L.K., Nathans D.;
RT "Cooperative transcriptional activity of Jun and Stat3 beta, a short
RT form of Stat3.";
RN Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=129/SvJ;
RX PubMed=1161809; DOI=10.1006/geno.2000.6433;
RA Miyoshi K., Cui Y., Riedlinger G., Lehoczy J., Zon L., Oka T.,
RA Dewar K., Hennighausen L.;
RT "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
RT zebrafish to mouse.";
RN Genomics 71:150-155(2001).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A).
RC STRAIN=C57BL/60, and NOD/LtJ;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.

RX MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
RA Wen Z., Zhong Z., Darnell J.E. Jr.;
RT "Maximal activation of transcription by Stat1 and Stat3 requires both
RT tyrosine and serine phosphorylation.";
RN Cell 82:241-250(1995).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
RX MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
RA Becker S., Groner B., Mueller C.W.;
RT "Three-dimensional structure of the Stat3beta homodimer bound to
RT DNA.";
RN Nature 394:145-151(1998).
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes. STAT3B interacts with the N-terminal
CC part of JUN to activate such promoters in a cooperative way.
CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOA1 (by similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Stat3A;
CC IsoId=P42227-1; Sequence=Displayed;
CC Name=Stat3B;
CC IsoId=P42227-2; Sequence=VSP_006287;
CC Name=Del-701;
CC IsoId=P42227-3; Sequence=VSP_010475;
CC -!- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
CC kidney. STAT3B is also detected in the liver, although in a much
CC less abundant manner.
CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L29278; AAA37254.1; -;
CC EMBL; U06922; AAA19452.1; -;
CC EMBL; U08378; AAA56668.1; -;
CC EMBL; U30709; AAC52612.1; -;
CC EMBL; AF246978; AAL59017.1; -;
CC EMBL; AY299489; AAQ75418.1; -;
CC EMBL; AY299490; AAQ75419.1; -;
CC EMBL; BC003806; AAH03806.1; -;
CC PIR; I49508; I49508.
CC PDB; 1BG1; X-ray; A=1-722.
CC TRANSFAC; T01574; -;
CC MGD; MGI:103038; Stat3.
CC GO; GO:0005737; Cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC GO; GO:0003677; F:DNA binding; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0016563; F:transcriptional activator activity; IDA.
CC GO; GO:0007259; P:JAK-STAT cascade; IDA.
CC GO; GO:0006357; P:regulation of transcription from Pol II pro. .; IDA.
CC InterPro; IPR008967; P53 like_DNA_bnd.
CC InterPro; IPR000980; SH2.
CC InterPro; IPR001217; STAT.
CC Pfam; PF00017; SH2; 1.
CC Pfam; PF01017; STAT_alpha; 1.
CC Pfam; PF02864; STAT_bind; 1.

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DR Pfam; PF02865; STAT int; 1.
DR PROSITE; PS50001; SH2; 1.
KW 3D-structure; Activator; Acute phase; Alternative splicing;
KW Direct protein sequencing; DNA-binding; Nuclear protein;
KW Phosphorylation; SH2 domain; Transcription regulation.
FT DOMAIN 580 670
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine.
FT VARSPPLIC 716 770 TTSNTIDLPMSPTLDSLMQFGNGEGAPSPAGGQFESLT
FT FMDLTSSECATSPM -> FIDAVWK (in isoform
FT Stat3B).
FT FTID=VSP_006287.
FT Missing (in isoform Del-701).
FT VARSPPLIC 701 701 /FTID=VSP_010475.
FT MUTAGEN 727 727 S->A: Decreased transcriptional
FT activation.
FT CONFLICT 16 16 E -> K (in Ref. 2).
FT CONFLICT 25 25 S -> T (in Ref. 2 and 4).
FT CONFLICT 394 394 M -> I (in Ref. 1).
FT HELIX 139 180
FT TURN 181 182
FT TURN 197 198
FT HELIX 199 237
FT TURN 238 238
FT HELIX 239 251
FT TURN 252 253
FT HELIX 261 290
FT TURN 294 295
FT TURN 297 301
FT HELIX 302 320
FT TURN 321 328
FT STRAND 330 331
FT TURN 333 334
FT TURN 336 337
FT STRAND 338 340
FT TURN 341 342
FT STRAND 345 351

Query Match 98.6%; Score 1156; DB 1; Length 770;
Best Local Similarity 98.7%; Pred. No. 3.1e-65;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHAQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDVVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 189

QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRPEI 120
DB 190 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRPEI 249

QY 121 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVSYGKDPPIVQHRPMLERI 180
DB 250 ACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVSYGKDPPIVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 3
STA3 RAT STANDARD; PRT; 770 AA.
AC P52631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 21-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name=Stat3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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STA3_BOVIN
ID STA3_BOVIN STANDARD; PRT; 770 AA.
AC Pe1635;
DT 05-JUL-2004 (Rel. 44, Created)
DT 25-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3.
GN Name-STAT3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
ON NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
RT "The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus during ruminant evolution."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various acute-phase protein genes (By similarity).
CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1). Interacts with NCOA1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC
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CC
CC EMBL; AJ620655; CAF06182.1; -.
DR PROSITE; PS5001; SH2; 1.
KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
FT Transcription regulation.
KW DOMAIN 580 670 SH2.
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
SQ SEQUENCE 770 AA; 87974 MW; 9CEB147C73B83274 CRC64;
Query Match 98.0%; Score 1149; DB 1; Length 770;
Best Local Similarity 98.3%; Pred. No. 8.6e-65;
Matches 225; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQMLEQHQADVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMODLN 60
DB 130 NHPTAAVTEKQMLEQHQADVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMODLN 189
QY 61 GNNQSVTRQKMQQLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQQLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNICLDLENWITSLSAQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERIV 180
DB 250 ACIGGPPNICLDLENWITSLSAQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERIV 309
QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 358
RESULT 5
Q6DV79
ID Q6DV79 PRELIMINARY; PRT; 771 AA.
AC Q6DV79;

DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Signal transducer and activator of transcription 3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
ON NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G.Y., Leung F.C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641397; AAT64887.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS5001; SH2; 1.
SQ SEQUENCE 771 AA; 88174 MW; 71AC855C5DC03E2 CRC64;
Query Match 96.5%; Score 1131; DB 2; Length 771;
Best Local Similarity 96.9%; Pred. No. 1.2e-63;
Matches 221; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 2 HPTAAVTEKQMLEQHQADVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMODLN 61
DB 131 HPTAAVTEKQMLEQHQADVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMODLN 190
QY 62 NNQSVTRQKMQQLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEIA 121
DB 191 NNQSVTRQKMQQLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEIA 250
QY 122 CIGGPPNICLDLENWITSLSAQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERIV 181
DB 251 CIGGPPNICLDLENWITSLSAQLOTRQOIKKLELOQKVS YKGDPIVQHRPMLERIV 310
QY 182 ELFRNLKMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 229
DB 311 ELFRNLKMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKFPPEL 358
RESULT 6
Q9PVX8
ID Q9PVX8 PRELIMINARY; PRT; 769 AA.
AC Q9PVX8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Stat 3.
GN Name-stat 3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
ON NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
RA Nishinakamura R., Matsumoto Y., Matsuda T., Ariizumi T., Heike T.,
RA Asashima M., Yokota T.;
RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
RT embryos independent of BMP-4."
RL Dev. Biol. 216:481-490(1999).
DR EMBL; AB017701; BAA86061.1; -.

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DR HSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2_1.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2_1.
DR PROSITE; PS50001; SH2_1.
SQ SEQUENCE 769 AA; 87974 MW; 0905C03263303069 CRC64;

Query Match 93.7%; Score 1098; DB 2; Length 769;
Best Local Similarity 92.6%; Pred. No. 1.5e-61;
Matches 212; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 NHPTAAVTEKQMLEQHAQDVVRKVDLEQKMKVVENLODDFDNFYKTLKSGQMDLN 60
Db 130 SHPNAAVTEKQMLEQHLQDVVRKVDLEQKMKVVENLODDFDNFYKTLKSGQDLSELN 189

Qy 61 GNNQSVTRQKQMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRPEI 120
Db 190 GNNQSVTRQKQMLEQMLTALDQMRRTIISDLASLLSAMEYVQKLTLDDELADWKRQOI 249

Qy 121 ACIGGPPNICLDRLENWITSLSAQLOTRQIKKLELOQKVSQKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLENWITSLSAQLOTRQIKKLELOQKVSQKGDPIVQHRPMLERI 309

Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLVKKPEL 229
Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLVKKPEL 358

RESULT 7
Q7ZXK3 PRELIMINARY; PRT; 766 AA.
AC Q7ZXK3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat3-A protein.
GN Name=stat3-A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;

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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative.";
RN Dev. Dyn. 225:384-391 (2002).
[3]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044717; AAH44717.1; -.
DR HSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2_1.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2_1.
DR PROSITE; PS50001; SH2_1.
SQ SEQUENCE 766 AA; 87599 MW; 31018A3321CCBB9C CRC64;

Query Match 93.4%; Score 1095; DB 2; Length 766;
Best Local Similarity 91.7%; Pred. No. 2.3e-61;
Matches 210; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy 1 NHPTAAVTEKQMLEQHAQDVVRKVDLEQKMKVVENLODDFDNFYKTLKSGQMDLN 60
Db 130 SHPNAAVTEKQMLEQHLQDVVRKVDLEQKMKVVENLODDFDNFYKTLKSGQDLSELN 189

Qy 61 GNNQSVTRQKQMLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTLDDELADWKRPEI 120
Db 190 GNNQSVTRQKQMLEQMLTALDQMRRTIISDLASLLSAMEYVQKLTLDDELADWKRQOI 249

Qy 121 ACIGGPPNICLDRLENWITSLSAQLOTRQIKKLELOQKVSQKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLENWITSLSAQLOTRQIKKLELOQKVSQKGDPIVQHRPMLERI 309

Qy 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLVKKPEL 229
Db 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLVKKPEL 358

RESULT 8
Q7ZTS5 PRELIMINARY; PRT; 414 AA.
AC Q7ZTS5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stat3 protein.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;

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RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN-AB; TISSUE-Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045276; AAH45276.1; -;
DR HSSP; P42227; 1BG1.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 414 AA; 48253 MW; 0FFD1B509B7526BD CRC64;

Query Match 86.2%; Score 1010; DB 2; Length 414;
Best Local Similarity 84.3%; Pred. No. 2.9e-56;
Matches 194; Conservative 21; Mismatches 13; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHAQDVKRVQDLQKQKVVENLQDDFDNFYKTLKSQDM-QDLN 60
DB 130 HPTGVVTEKQQLLEHNLQDQIRKRVQDMQKMLENLQDDFDNFYKTLKSAGEISQDLN 189
QY 61 GNNQ-SVTRQKMQQLEQMLTALDQMRSSIVSELGALLSMEYVQKTLTDEELADWKRRPE 119
DB 190 GNSAAATRQKMSQLEQMLSDQLRRQIVTEMAGLSAMDVFQKNLTDEELADWKRRQ 249
QY 120 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQSVYKGDPIVQHRPMLER 179
DB 250 IACIGPPNICLDRLTWTSLAESQLQIRQIKLEELQKQSVYKGDPIIHRPALEBK 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 229
DB 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 359

RESULT 9
Q6DVF3
ID Q6DVF3 PRELIMINARY; PRT; 765 AA.
AC Q6DVF3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Signal transducer and activation of transcription factor 3.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RL Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY639947; AAT64912.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 765 AA; 87566 MW; F5D01408748EC703 CRC64;
Query Match 86.2%; Score 1010; DB 2; Length 765;
Best Local Similarity 84.3%; Pred. No. 5.6e-56;
Matches 194; Conservative 20; Mismatches 14; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEQHAQDVKRVQDLQKQKVVENLQDDFDNFYKTLKSQDM-QDLN 60
DB 130 HPTGVVTEKQQLLEHNLQDQIRKRVQDMQKMLENLQDDFDNFYKTLKSQELNQLN 189
QY 61 GNNQ-SVTRQKMQQLEQMLTALDQMRSSIVSELGALLSMEYVQKTLTDEELADWKRRPE 119
DB 190 GNSAAATRQKMSQLEQMLSDQLRRQIVTEMAGLLTAMDYVQKNLTDEELADWKRRQ 249
QY 120 IACIGPPNICLDRLNWTSLAESQLQTRQIKLEELQKQSVYKGDPIVQHRPMLER 179
DB 250 IACIGPPNICLDRLTWTSLAESQLQIRQIKLEELQKQSVYKGDPIIHRPALEBK 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 229
DB 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVKTGQVFTTKVRLLVKFPPEL 359
RESULT 10
Q6GUE7
ID Q6GUE7 PRELIMINARY; PRT; 785 AA.
AC Q6GUE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Signal transducer and activator of transcription 3 isoform 1.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RL Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641434; AAT46364.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.

DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 785 AA; 89643 MW; 81F231BDE27DE938 CRC64;

Query Match 86.2%; Score 1010; DB 2; Length 785;
Best Local Similarity 84.3%; Pred. No. 5.7e-56;
Matches 194; Conservative 20; Mismatches 14; Indels 2; Gaps 2;

QY 2 HPTAAVTEKQMLEQHAQDVQRKVDLEQKMKVVENLQDDFDNFYKTLKSQGM-QDNLN 60
DB 130 HPTGTVVTEKQMLEHNLQDRIKRVQDMEQKMKLENLQDDFDNFYKTLKSQGLNQLN 189
QY 61 GNNQ-SVTRQKMOLEQMLTALDQMRISIVSELAGLLSAMEYVOKLTIDELADWKRPE 119
DB 190 GNSQAAATRQKMALEQMLTALDQMRISIVSELAGLLSAMEYVOKLTIDELADWKRQ 249
QY 120 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKVKYKGDPIVQHRPMLER 179
DB 250 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKVKYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229
DB 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 359

RESULT 11
Q6NV46 PRELIMINARY; PRT; 786 AA.
AC Q6NV46;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Stat3 protein.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC068320; AAHG8320.1; -;
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR Pfam; PF00117; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 786 AA; 90039 MW; FC7371D0B0E5447E CRC64;

Query Match 86.2%; Score 1010; DB 2; Length 786;
Best Local Similarity 84.3%; Pred. No. 5.7e-56;
Matches 194; Conservative 21; Mismatches 13; Indels 2; Gaps 2;

QY 2 HPTAAVTEKQMLEQHAQDVQRKVDLEQKMKVVENLQDDFDNFYKTLKSQGM-QDNLN 60
DB 130 HPTGTVVTEKQMLEHNLQDRIKRVQDMEQKMKLENLQDDFDNFYKTLKSAGLSQDLN 189
QY 61 GNNQ-SVTRQKMOLEQMLTALDQMRISIVSELAGLLSAMEYVOKLTIDELADWKRPE 119
DB 190 GNSQAAATRQKMSQLEQMLTALDQMRISIVSELAGLLSAMEYVOKLTIDELADWKRQ 249
QY 120 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKVKYKGDPIVQHRPMLER 179
DB 250 IACIGGPPNICLDRLNWTSLAESQLQTRQIKKLELQKVKYKGDPIVQHRPMLER 309
QY 180 IVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 229
DB 310 IVDLFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEL 359

RESULT 12
O93599 PRELIMINARY; PRT; 806 AA.
AC O93599;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcription factor.
GN Name=stat3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Oates A.C.;
RL Thesis (1998); University of Melbourne, Australia.
DR EMBL; AJ005693; CAA06677.1; -;
DR HSSP; P42227; IBGI.
DR ZFIN; ZDB-GENE-980526-68; stat3.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;

Query Match 86.2%; Score 1010; DB 2; Length 806;
Best Local Similarity 84.3%; Pred. No. 5.9e-56;

Matches 194; Conservative 21; Mismatches 13; Indels 2; Gaps 2;

QY 2 HPTAAVTEKQMLEHQAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSQGDMD-QDLN 60
Db 130 HPTGTVTEKQMLEHQAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSQGDMD-QDLN 189

QY 61 GNNQ-SVTRQKMOQLEMLTALDOMRRIISVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEMLTALDOMRRIISVSELAGLLSAMEYVQKTLTDEELADWKRRQ 249

QY 120 IACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEELQKVSXKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEELQKVSXKGDPIVQHRPMLER 309

QY 180 IVELFRNLKMSAFVVERQPCMPHDPDRPLVIKTVQFTTKVRLLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPDRPLVIKTVQFTTKVRLLVKFPPEL 359

RESULT 13

Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16; (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphia; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF001017; SH2; 1.
DR Pfam; PF02864; STAT_alpha; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS50001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; B661PFE18B8FDB8E CRC64;

Query Match 84.1%; Score 986; DB 2; Length 764;
Best Local Similarity 83.0%; Pred. No. 1.8e-54;
Matches 191; Conservative 21; Mismatches 16; Indels 2; Gaps 2;

QY 2 HPTAAVTEKQMLEHQAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSQGDMD-QDLN 60
Db 130 NPSTGTVTEKQMLEHQAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSQGDMD-QDLN 189

QY 61 GNNQ-SVTRQKMOQLEMLTALDOMRRIISVSELAGLLSAMEYVQKTLTDEELADWKRRPE 119
Db 190 GNSQAARQKMAQLEMLTALDOMRRIISVSELAGLLSAMEYVQKTLTDEELADWKRRQ 249

QY 120 IACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEELQKVSXKGDPIVQHRPMLER 179
Db 250 IACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEELQKVSXKGDPIVQHRPMLER 309

QY 180 IVELFRNLKMSAFVVERQPCMPHDPDRPLVIKTVQFTTKVRLLVKFPPEL 229
Db 310 IVDLFRNLKMSAFVVERQPCMPHDPDRPLVIKTVQFTTKVRLLVKFPPEL 359

RESULT 14

O13133 PRELIMINARY; PRT; 767 AA.
AC O13133; (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
GN Names:rbStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AAB60926.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;

Query Match 83.3%; Score 976; DB 2; Length 767;
Best Local Similarity 81.0%; Pred. No. 8e-54;
Matches 187; Conservative 25; Mismatches 17; Indels 2; Gaps 2;

QY 1 NHPTAAVTEKQMLEHQAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSQGDMD-QDL 59
Db 129 SHPSGTVTEKQMLEHQAQDVRRKVDLEQKMKVVENLQDDFDNFYKTLKSQGDMD-QDL 188

QY 60 GNNQ-SVTRQKMOQLEMLTALDOMRRIISVSELAGLLSAMEYVQKTLTDEELADWKRRP 118
Db 189 GNSQAARQKMAQLEMLTALDOMRRIISVSELAGLLSAMEYVQKTLTDEELADWKRRQ 248

QY 119 ETACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEELQKVSXKGDPIVQHRPMLER 178
Db 249 QIACIGGPPNICLDRLNWTSLAESQLQTRQOIKKLEELQKVSXKGDPIVQHRPMLER 308

QY 179 RIVELFRNLKMSAFVVERQPCMPHDPDRPLVIKTVQFTTKVRLLVKFPPEL 229
Db 309 KIVDLFRNLKMSAFVVERQPCMPHDPDRPLVIKTVQFTTKVRLLVKFPPEL 359

RESULT 15

O9N145 PRELIMINARY; PRT; 163 AA.
AC O9N145; (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Signal transducer and activator of transcription (Fragment).
GN Name-STAT3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Arredondo J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF227560; AAF73401.1; -.
DR HSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR001217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
FT NON_TER 1
FT TER 163
SQ SEQUENCE 163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;

Query Match 56.0%; Score 656; DB 2; Length 163;
Best Local Similarity 98.4%; Pred. No. 2.9e-34;
Matches 126; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 102 VQKTLTDEELADWKRRPEIACIGPPNICLDRLNWTSLAESQLQTRQIQKLELQOK 161
Db 1 VQKTLTDEELADWKRRQIQIACIGPPNICLDRLNWTSLAESQLQTRQIQKLELQOK 60

Qy 162 VSYKGDPIVQHRPMLERIIVELFRLNLMKSAFVVERQPCMPMPDRPLVIKIGVQFTTKVR 221
Db 61 VSYKGDPIVQHRPMLERIIVELFRLNLMKSAFVVERQPCMPMPDRPLVIKIGVQFTTKVR 120

Qy 222 LLVKFPPEL 229
Db 121 LLVKFPPEL 128

Search completed: May 25, 2005, 17:43:44
Job time : 96.284 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:14:45 ; Search time 121.891 Seconds
(without alignments)
726.619 Million cell updates/sec

Title: US-10-090-185-31

Perfect score: 1172

Sequence: 1 NHPAAVTEKQMLSEQLQ.....IKTGVOFTTKVRLLVKFPPEL 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1172	100.0	229	4 AAY72863	Aay72863 Mouse Sta
2	1168	99.7	229	4 AAY72850	Aay72850 Mouse Sta
3	1168	99.7	252	4 AAY72846	Aay72846 Mouse Sta
4	1168	99.7	271	4 AAY72841	Aay72841 Mouse Sta
5	1168	99.7	770	2 AAY72082	Aar72082 Mouse Sta
6	1168	99.7	770	2 AAW03176	Aaw03176 Mouse Sta
7	1163	99.2	229	4 AAY72862	Aay72862 Mouse Sta
8	1157.5	98.8	228	4 AAY72861	Aay72861 Mouse Sta
9	1157	98.7	720	5 AAE22055	Aae22055 Human Sta
10	1157	98.7	769	5 ABB57164	Abb57164 Mouse isc
11	1157	98.7	769	5 AAE22054	Aae22054 Human Sta
12	1157	98.7	769	5 AAE22056	Aae22056 Human pro
13	1157	98.7	770	2 AAR82995	Aar82995 Mouse liv
14	1157	98.7	770	2 AAY03768	Aay03768 Human STA
15	1157	98.7	770	3 AAB12377	Aab12377 N-termina
16	1157	98.7	770	5 AAE14652	Aae14652 Murine ST
17	1157	98.7	770	5 ABG69497	Abg69497 Human bai
18	1157	98.7	770	6 ABUI0476	Abui0476 Mouse STA
19	1157	98.7	770	8 ADN04365	Adn04365 Antipsori
20	1157	98.7	770	8 ADP54789	Adp54789 Human PRO
21	1157	98.7	793	3 AAB58442	Aab58442 Lung canc
22	1154	98.5	770	7 ADD44738	Add44738 Rat Prote
23	1152	98.3	770	2 AAR82993	Aar82993 Human pla
24	1152	98.3	770	4 AAB19964	Aab19964 Human sig
25	1152	98.3	770	5 AAE15174	Aae15174 Human Sta

26	1152	98.3	770	7	ADD44740	Add44740 Human Pro
27	1150	98.1	229	4	AAY72860	Aay72860 Mouse Sta
28	1090	93.0	213	4	AAY72851	Aay72851 Mouse Sta
29	1090	93.0	236	4	AAY72847	Aay72847 Mouse Sta
30	1044	89.1	223	4	AAY72854	Aay72854 Mouse Sta
31	845	72.1	185	4	AAY72855	Aay72855 Mouse Sta
32	777	66.3	176	4	AAY72848	Aay72848 Mouse Sta
33	653	55.7	128	4	AAY72852	Aay72852 Mouse Sta
34	601	51.3	143	4	AAY72849	Aay72849 Mouse Sta
35	573	48.9	749	5	AAG78526	Aag78526 Rat STAT-
36	571	48.7	129	4	AAY72856	Aay72856 Mouse Sta
37	569	48.5	268	4	AAY72844	Aay72844 Mouse Sta
38	569	48.5	582	2	AAW62996	Aaw62996 Human tru
39	569	48.5	582	6	ABU04748	Abu04748 Human exp
40	569	48.5	582	8	ADH57036	Adh57036 Truncated
41	569	48.5	680	6	ABR59713	Abr59713 Human sig
42	569	48.5	712	2	AAR72079	Aar72079 Human sig
43	569	48.5	712	2	AAW03170	Aaw03170 Human STA
44	569	48.5	712	2	AAW62995	Aaw62995 Human STA
45	569	48.5	712	6	ABU04747	Abu04747 Human exp

ALIGNMENTS

RESULT 1

AAV72863

ID AAY72863 standard; protein; 229 AA.

AC AAY72863;

DT 31-MAY-2001 (first entry)

DE Mouse Stat3 mutant (V151A) protein fragment (130-358 amino acids).

XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;

KW cellular transformation; dysproliferative disease; cancer; psoriasis;

XX therapy; mutant; mutuin.

OS Mus musculus.

Key Location/Qualifiers

Region 1..25

FT /note= "Stat3-c-Jun interaction region 1; corresponds to

130-154 position of Stat3 protein"

FT Misc-difference 22

FT /note= "wild type Val substituted with Ala corresponds to

151 position of Stat-3 protein"

FT Region 213..229

FT /note= "Stat3-c-Jun interaction region 2; corresponds to

342-358 position of Stat3 protein"

PN WO200116605-A2.

PD 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US023822.

PR 31-AUG-1999; 99US-00387418.

XX (UYRQ) UNIV ROCKEFELLER.

XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;

DR WPI; 2001-226705/23.

XX Identifying an agent for use in modulating the interaction between

transcription factor c-Jun and a Stat3 protein.

XX Claim 66; Page 86; 86pp; English.

XX The present sequence is mouse Stat3 mutant (V151A) protein fragment

CC containing 130-358 amino acids of Stat3 protein. This mutant is obtained

CC

CC by replacing Val 151 with Ala in Stat3 protein. The invention relates to
 CC methods for identifying interacting regions of transcription factors and
 CC methods for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 CC
 XX Sequence 229 AA;

Query Match 100.0%; Score 1172; DB 4; Length 229;
 Best Local Similarity 100.0%; Pred. No. 6.5e-100;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
 DB 1 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLEELQKVKSGDPIVQHRPMLERI 180
 DB 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLEELQKVKSGDPIVQHRPMLERI 180
 QY 181 VELFRNLMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
 DB 181 VELFRNLMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 2
 AAY72850
 ID AAY72850 standard; protein; 229 AA.

XX AAY72850;
 AC
 DE 31-MAY-2001 (first entry)
 XX Mouse Stat3 protein fragment #8 (130-358 amino acids).
 XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX Mus musculus.
 XX Key Location/Qualifiers
 FH Region 1. .25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Region 213. .229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX WO200116605-A2.

XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 DR WPI; 2001-226705/23.
 XX Identifying an agent for use in modulating the interaction between
 PT transcription factor c-Jun and a Stat3 protein.

XX Claim 65; Page 76-77; 86pp; English.
 PS The present sequence is mouse Stat3 protein fragment containing 130-358
 CC amino acids of Stat3 protein. This Stat3 fragment showed strong binding
 CC to c-Jun protein in the cell extract. The invention relates to methods
 CC for identifying interacting regions of transcription factors and methods
 CC for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 CC
 XX Sequence 229 AA;

Query Match 99.7%; Score 1168; DB 4; Length 229;
 Best Local Similarity 99.6%; Pred. No. 1.5e-99;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
 DB 1 NHPTAAVVTKEQKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
 QY 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 61 GNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLEELQKVKSGDPIVQHRPMLERI 180
 DB 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKLEELQKVKSGDPIVQHRPMLERI 180
 QY 181 VELFRNLMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
 DB 181 VELFRNLMSAFVVERQPCMPMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229

RESULT 3
 AAY72846
 ID AAY72846 standard; protein; 252 AA.

XX AAY72846;
 AC
 DE 31-MAY-2001 (first entry)
 XX Mouse Stat3 protein fragment #4 (107-358 amino acids).
 XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;
 KW therapy.
 XX Mus musculus.
 XX Key Location/Qualifiers
 FH Region 24. .48
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT Region 236. .252
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX WO200116605-A2.

XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;

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XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX
XX Claim 65; Page 73; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 107-358
XX amino acids of Stat3 protein. This Stat3 fragment showed strong binding
XX to c-Jun protein in the cell extract. The invention relates to methods
XX for identifying interacting regions of transcription factors and methods
XX for identifying agents which modulates the interaction between a
XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
XX Stat-3, useful for modulating gene transcription e.g., cellular
XX transformation. These identifying agents are used in the treatment of
XX dysproliferative diseases and also for treating cancer and psoriasis. A
XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
XX binding domain, linker domain, SH2 domain and transactivation domain
XX
XX Sequence 252 AA;
XX
XX Query Match 99.7%; Score 1168; DB 4; Length 252;
XX Best Local Similarity 99.6%; Pred. No. 1.7e-99;
XX Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 60
XX Db 24 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 83
XX
XX QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRRPEI 120
XX Db 84 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRRPEI 143
XX
XX QY 121 ACIGGPPNICLDRLENWITSLAESQLQTRQIQKLEELQKYSYKGDPIVQHRPMLLEERI 180
XX Db 144 ACIGGPPNICLDRLENWITSLAESQLQTRQIQKLEELQKYSYKGDPIVQHRPMLLEERI 203
XX
XX QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEEL 229
XX Db 204 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEEL 252
XX
XX RESULT 4
XX AAY72841
XX ID AAY72841 standard; protein; 271 AA.
XX AC AAY72841;
XX
XX DT 31-MAY-2001 (first entry)
XX
XX DE Mouse Stat3 protein fragment #2 (107-377 amino acids).
XX
XX KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
XX cellular transformation; dysproliferative disease; cancer; psoriasis;
XX therapy.
XX
XX OS Mus musculus.
XX
XX FH Key Location/Qualifiers
XX FT Region 24..48
XX FT /notes="Stat3-c-Jun interaction region 1; corresponds to
XX FT 130-154 position of Stat3 protein"
XX FT Region 236..252
XX FT /note="Stat3-c-Jun interaction region 2; corresponds to
XX FT 342-358 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX PN 08-MAR-2001.
XX
XX PD
XX
XX PF 30-AUG-2000; 2000WO-US023822.
XX

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PR 31-AUG-1999; 99US-00387418.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wzrzeszczynska MH, Darnell JE;
XX
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein.
XX
XX Claim 65; Page 67-68; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 107-377
XX amino acids of Stat3 protein. This Stat3 fragment showed strong binding
XX to c-Jun protein in the cell extract. The invention relates to methods
XX for identifying interacting regions of transcription factors and methods
XX for identifying agents which modulates the interaction between a
XX transcription factor such as c-Jun and a Stat protein such as Stat-1 and
XX Stat-3, useful for modulating gene transcription e.g., cellular
XX transformation. These identifying agents are used in the treatment of
XX dysproliferative diseases and also for treating cancer and psoriasis. A
XX Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
XX binding domain, linker domain, SH2 domain and transactivation domain
XX
XX Sequence 271 AA;
XX
XX Query Match 99.7%; Score 1168; DB 4; Length 271;
XX Best Local Similarity 99.6%; Pred. No. 1.9e-99;
XX Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 60
XX Db 24 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDFDFNYKTLKSGQDMQDLN 83
XX
XX QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRRPEI 120
XX Db 84 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDBELADWKRRPEI 143
XX
XX QY 121 ACIGGPPNICLDRLENWITSLAESQLQTRQIQKLEELQKYSYKGDPIVQHRPMLLEERI 180
XX Db 144 ACIGGPPNICLDRLENWITSLAESQLQTRQIQKLEELQKYSYKGDPIVQHRPMLLEERI 203
XX
XX QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEEL 229
XX Db 204 VELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKPEEL 252
XX
XX RESULT 5
XX AAR72082
XX ID AAR72082 standard; protein; 770 AA.
XX
XX AC AAR72082;
XX
XX DT 25-MAR-2003 (revised)
XX DT 27-SEP-1995 (first entry)
XX
XX DE Mouse Stat3 (198f6).
XX
XX KW Signal transducer and activator of transcription; STAT; 198f6; Stat3;
XX receptor recognition factor; transcription factor; cellular debilitation;
XX derangement; dysfunction; interferon-gamma.
XX
XX OS Mus sp.
XX
XX PN WO9508629-A1.
XX
XX PD 30-MAR-1995.
XX
XX PF 26-SEP-1994; 94WO-US010849.
XX
XX PF 24-SEP-1993; 93US-00126588.
XX
XX PR 24-SEP-1993; 93US-00126595.

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PR 11-MAR-1994; 94US-00212184.
PR 11-MAR-1994; 94US-00212185.
XX PA (UYRQ) UNIV ROCKEFELLER.
XX Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
XX WPI; 1995-139598/18.
DR N-PSDB; AAQ89340.
XX Receptor recognition factor implicated in transcriptional stimulation of
PT genes - useful in drug screening assays and/or for treating cellular
PT debilitations, derangements and/or dysfunctions, etc.
XX Claim 1; Page 107-110; 160pp; English.
PS A fragment encoding the human Stat91 protein was used to screen a murine
CC thymus and spleen cDNA for homologous proteins. A highly homologous gene
CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)
CC (Stat1) that was responsive to interferon- gamma. Using a fragment of the
CC mouse gene as probe, 2 additional members of the 113-91 family of
CC receptor recognition factor proteins were isolated. The 2 genes (AAQ89339
CC -40) were cloned in plasmids 136f1 and 19sf6 and encoded proteins termed
CC Stat4 (AAR72081) and Stat3 (AAR72082), respectively. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 770 AA;
Query Match 99.7%; Score 1168; DB 2; Length 770;
Best Local Similarity 99.6%; Pred. No. 7.5e-99;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVODLEQKMKVVENLODDPFDNFYKTLKSGDMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDARKRVODLEQKMKVVENLODDPFDNFYKTLKSGDMQDLN 189
QY 61 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVOKLTLDDELADWKRRPEI 120
Db 190 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVOKLTLDDELADWKRRPEI 249
QY 121 ACIGGPNICLDRLNWIITSLAESQLQTRQIQIKKLEELQOKVSYKGDPIVQHRPMLERI 180
Db 250 ACIGGPNICLDRLNWIITSLAESQLQTRQIQIKKLEELQOKVSYKGDPIVQHRPMLERI 309
QY 181 VELFRNLKSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPPPEL 229
Db 310 VELFRNLKSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPPPEL 358
RESULT 6
AAW03176
XX AAW03176 standard; protein; 770 AA.
XX
AC AAW03176;
XX
DT 24-OCT-1996 (first entry)
XX
DE Mouse STAT4.
XX
KW STAT; STAT4; signal transducer and activator of transcription;
KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;
KW autoimmune disease; antagonist; therapy.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
XX 398..508
FT Domain /label= DNA binding domain
FT /note= "Claim 3, page 110"
XX
XX WO9620954-A2.
XX
XX 11-JUL-1996.

XX 28-DEC-1995; 95WO-USO17025.
PF
XX
PR 06-JAN-1995; 95US-00369796.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Darnell JE, Wen Z, Horvath CM, Zhong Z;
XX
XX WPI; 1996-333941/33.
DR N-PSDB; AAT311280.
XX New STAT protein DNA-binding domain peptide(s) - useful for diagnosing,
PT preventing or treating cellular dysfunction, e.g. oncogenesis,
PT inflammation, parasitic disease or autoimmunity.
XX
PS Disclosure; Page 87-90; 138pp; English.
XX Mouse signal transducer and activator of transcription (STAT) protein
CC STAT4 (AAW03176) serves a dual purpose, i.e. signal transduction from
CC ligand-activated receptor kinase complexes followed by nuclear
CC translocation and DNA binding to activate transcription. Recombinant
CC STAT4 can be obt'd. using cDNA clone 19sf6 (AAT31278) obt'd. from
CC splenic/thymic cells. STAT4 includes a DNA-binding domain (see also
CC AAW03167) capable of both receptor recognition and message delivery via
CC DNA binding in a receptor-ligand specific manner. STAT proteins and their
CC DNA binding domains (see also AAW03165-75) are useful for screening
CC antagonists used to inhibit STAT-mediated signal transduction and
CC activation of transcription
XX
SQ Sequence 770 AA;
Query Match 99.7%; Score 1168; DB 2; Length 770;
Best Local Similarity 99.6%; Pred. No. 7.5e-99;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVODLEQKMKVVENLODDPFDNFYKTLKSGDMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDARKRVODLEQKMKVVENLODDPFDNFYKTLKSGDMQDLN 189
QY 61 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVOKLTLDDELADWKRRPEI 120
Db 190 GNNQSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMEYVOKLTLDDELADWKRRPEI 249
QY 121 ACIGGPNICLDRLNWIITSLAESQLQTRQIQIKKLEELQOKVSYKGDPIVQHRPMLERI 180
Db 250 ACIGGPNICLDRLNWIITSLAESQLQTRQIQIKKLEELQOKVSYKGDPIVQHRPMLERI 309
QY 181 VELFRNLKSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPPPEL 229
Db 310 VELFRNLKSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPPPEL 358
RESULT 7
AAW72862
ID AAY72862 standard; protein; 229 AA.
XX
AC AAY72862;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 mutant (L148A) protein fragment (130-358 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy; mutant; muten.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
XX 1..25
FT Region /note= "Stat3-c-Jun interaction region 1; corresponds to
FT 130-154 position of Stat3 protein"
FT

FT Misc-difference 19 /note= "Wild type Leu substituted with Ala; corresponds
 FT /note= "Wild type Leu substituted with Ala; corresponds
 FT 213. .229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 XX
 PN WO200116605-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023822.
 XX
 PR 31-AUG-1999; 99US-00387418.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 XX
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 DR
 XX Identifying an agent for use in modulating the interaction between
 FT transcription factor c-Jun and a Stat3 protein.
 FT
 XX Claim 66; Page 85; 86pp; English.

XX The present sequence is mouse Stat3 mutant (L148A) protein fragment
 CC containing 130-358 amino acids of Stat3 protein. This mutant is obtained
 CC by replacing Leu 148 with Ala in Stat3 protein. The invention relates to
 CC methods for identifying interacting regions of transcription factors and
 CC methods for identifying agents which modulates the interaction between a
 CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and
 CC Stat-3, useful for modulating gene transcription e.g., cellular
 CC transformation. These identifying agents are used in the treatment of
 CC dysproliferative diseases and also for treating cancer and psoriasis. A
 CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA
 CC binding domain, linker domain, SH2 domain and transactivation domain
 XX
 SQ Sequence 229 AA;

Query Match 99.2%; Score 1163; DB 4; Length 229;
 Best Local Similarity 99.1%; Pred. No. 4.4e-99;
 Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 NHPTAAVVTKEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
 DB 1 NHPTAAVVTKEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
 QY 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDBELADWKRPEI 120
 DB 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDBELADWKRPEI 120
 QY 121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLEREI 180
 DB 121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLEREI 180
 QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVGTQFTTKVRLLVKPEL 229
 DB 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVGTQFTTKVRLLVKPEL 229

RESULT 8
 ID AAY72861
 XX AAY72861 standard; protein; 228 AA.
 AC AAY72861;
 XX
 DT 31-MAY-2001 (first entry)
 DE Mouse Stat3 mutant (T346A, K348A, R350A) protein fragment.
 XX
 KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
 KW cellular transformation; dysproliferative disease; cancer; psoriasis;

KW therapy; mutant; mutein.
 XX Mus musculus.
 XX
 XX Key Location/Qualifiers
 FT Region 1. .25
 FT /note= "Stat3-c-Jun interaction region 1; corresponds to
 FT 130-154 position of Stat3 protein"
 FT 213. .229
 FT /note= "Stat3-c-Jun interaction region 2; corresponds to
 FT 342-358 position of Stat3 protein"
 FT Misc-difference 217
 FT /note= "Wild type Thr substituted with Ala; corresponds
 FT to 346 position of Stat-3 protein"
 FT Misc-difference 219
 FT /note= "Wild type Lys substituted with Ala; corresponds
 FT to 348 position of Stat-3 protein"
 FT Misc-difference 221
 FT /note= "Wild type Arg substituted with Ala; corresponds
 FT to 350 position of Stat-3 protein"

XX WO200116605-A2.
 XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023822.
 XX 31-AUG-1999; 99US-00387418.
 XX (UYRQ) UNIV ROCKEFELLER.
 XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
 XX WPI; 2001-226705/23.
 DR
 XX Identifying an agent for use in modulating the interaction between
 FT transcription factor c-Jun and a Stat3 protein.
 FT
 XX Claim 66; Page 84-85; 86pp; English.

XX The present sequence is mouse Stat3 mutant protein fragment containing
 CC 130-358 amino acids of Stat3 protein. This mutant is obtained by
 CC replacing Thr 346 with Ala, Lys 348 with Ala and Arg 350 with Ala in the
 CC Stat3 protein. The invention relates to methods for identifying
 CC interacting regions of transcription factors and methods for identifying
 CC agents which modulates the interaction between a transcription factor
 CC such as c-Jun and a Stat protein such as Stat-1 and Stat-3, useful for
 CC modulating gene transcription e.g., cellular transformation. These
 CC identifying agents are used in the treatment of dysproliferative diseases
 CC and also for treating cancer and psoriasis. A Stat protein comprises the
 CC N-terminal domain, coiled-coil domain, DNA binding domain, linker domain,
 CC SH2 domain and transactivation domain
 XX
 SQ Sequence 228 AA;

Query Match 98.8%; Score 1157.5; DB 4; Length 228;
 Best Local Similarity 99.6%; Pred. No. 1.4e-98;
 Matches 228; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 NHPTAAVVTKEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
 DB 1 NHPTAAVVTKEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 59
 QY 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDBELADWKRPEI 120
 DB 60 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELQGLLSAMEYVQKTLTDBELADWKRPEI 119
 QY 121 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLEREI 180
 DB 120 ACIGGPPNICLDRLNWNITSLAESQLQTRQOIKKLEELQOKVSYKGDPIVQHRPMLEREI 179
 QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVGTQFTTKVRLLVKPEL 229

Db 180 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQFTTKVRLLVKPPPEL 228

RESULT 9

AAE22055

ID AAE22055 standard; protein; 720 AA.

AC AAE22055;

XX

XX 25-JUL-2002 (first entry)

DT

XX Human Stat3beta protein.

DE

XX Human; signal transducer and activator of transcription 3; ischaemia;

KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;

KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;

KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;

KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;

KW shock; chronic active hepatitis; adult respiratory distress syndrome;

KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;

KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;

KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;

KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;

KW carcinoma; degenerative disorder; gene therapy; growth deficiency;

KW cirrhosis; hypoproliferative disorder; lesion; Statbeta.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Misc-difference 713..714

FT /note= "Encoded by ACA CCA TTC"

FT

XX WO200220032-A1.

FN

XX 14-MAR-2002.

PD

XX 10-SEP-2001; 2001WO-US028254.

PF

XX 08-SEP-2000; 2000US-0231212P.

PR

XX (UYJO) UNIV JOHNS HOPKINS.

PA (UYSF-) UNIV SOUTH FLORIDA.

PA

XX Yu H, Pardoll D, Jove R, Dalton W;

PI

XX WPI; 2002-362218/39.

DR

XX N-PSDB; AAD35066.

DR

XX Modulating angiogenesis and an immune response in an individual, for

XX treating a hypoxic or ischemic condition, comprises administering a

PT compound that modulates the activity of a signal transducer and activator

PT of transcription 3.

PT

XX Disclosure; Page 87-89; 94pp; English.

PS

XX The invention relates to a method of modulating angiogenesis and immune

CC response. Method involves administering to an individual a compound that

CC modulate the activity of signal transducer and activator of transcription

CC 3 (Stat3). Modulating angiogenesis is useful for treating or preventing

CC hypoxic or ischaemic condition or disorder which is the result of stroke,

CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,

CC tissue ischaemia in the lower extremities, infarction, trauma, vascular

CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,

CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,

CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,

CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy

CC with neovascularisation. Suppressing an immune response is useful for

CC ameliorating a symptom of an autoimmune disease such as systemic lupus

CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,

CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,

CC mixed connective tissue disease, primary biliary cirrhosis, pernicious

CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,

CC gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis,

CC

CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's

CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune

CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and

CC dense deposit disease. The method is useful in preventing or treating

CC specific proliferative and oncogenic disease which includes sarcomas and

CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,

CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,

CC hypoproliferative disorders, physical trauma, lesions and wounds. The

CC method is also used in gene therapy. The present sequence is human

CC Stat3beta protein

XX

SQ Sequence 720 AA;

Query Match 98.7%; Score 1157; DB 5; Length 720;

Best Local Similarity 98.7%; Pred. No. 7.2e-98;

Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDARKRVODLEQMKVVENLODDFDNYKTLKSQGMODLN 60

Db 130 NHPTAAVTEKQOMLEQHLQDARKRVODLEQMKVVENLODDFDNYKTLKSQGMODLN 189

QY 61 GNNQSVTRQMKQOQLEQMLTALQDMRRSIVSELAGLISAMEYVQKTLTDBELADWKRRPEI 120

Db 190 GNNQSVTRQMKQOQLEQMLTALQDMRRSIVSELAGLISAMEYVQKTLTDBELADWKRRQOI 249

QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKKLEELQOKVSYKGDPIVQHRPMLLEERI 180

Db 250 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQIKKLEELQOKVSYKGDPIVQHRPMLLEERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQFTTKVRLLVKPPPEL 229

Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVKTGQFTTKVRLLVKPPPEL 358

RESULT 10

ABB57164

ID ABB57164 standard; protein; 769 AA.

XX

XX ABB57164;

XX

XX 07-MAR-2002 (first entry)

DT

XX Mouse ischaemic condition related protein sequence SEQ ID NO:398.

DE

XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

KW vasospastic ischaemia; ischaemic condition; ischaemic disease.

KW

XX Mus musculus.

OS

XX WO200188188-A2.

PN

XX 22-NOV-2001.

PD

XX 18-MAY-2001; 2001WO-JP004192.

PF

XX 18-MAY-2000; 2000JP-00145977.

PR

XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

PA

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.

DR

XX N-PSDB; ABI99454.

DR

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring

PT expression levels of particular genes defined in the specification or by

PT determining the expression profile of a gene group comprising these

PT genes.

XX

XX Claim 2; Page 1084-1087; 2690pp; English.

PS

XX The present invention describes a method for examining ischaemic

XX conditions, comprising measuring the expression levels of particular

CC

KW Human; signal transducer and activator of transcription 3; ischaemia;
KW immune response; Stat3; coronary atherosclerosis; vascular occlusion;
KW hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia;
KW inflammation; chronic obstructive pulmonary disease; cardiac arrest;
KW insulin dependent diabetes mellitus; emphysema; trauma; scleroderma;
KW shock; chronic active hepatitis; adult respiratory distress syndrome;
KW nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis;
KW Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy;
KW polymyositis; rheumatoid arthritis; autoimmune infertility; anaemia;
KW proliferative disease; Grave's disease; ulcerative colitis; sarcoma;
KW carcinoma; degenerative disorder; gene therapy; growth deficiency;
KW cirrhosis; hypoproliferative disorder; lesion.
OS Homo sapiens.
XX
XX
XX WO200220032-A1.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028254.
XX
XX 08-SEP-2000; 2000US-0231212P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX (UYSF-) UNIV SOUTH FLORIDA.
XX
XX Yu H, Pardoll D, Jove R, Dalton W;
XX
XX WPI; 2002-362218/39.
XX

Modulating angiogenesis and an immune response in an individual, for
treating a hypoxic or ischemic condition, comprises administering a
compound that modulates the activity of a signal transducer and activator
of transcription 3.
XX
XX Disclosure; Page 83-85; 94pp; English.

The invention relates to a method of modulating angiogenesis and immune
response. Method involves administering to an individual a compound that
modulate the activity of signal transducer and activator of transcription
3 (Stat3). Modulating angiogenesis is useful for treating or preventing
CC hypoxic or ischaemic condition or disorder which is the result of stroke,
CC ischaemia, coronary atherosclerosis, myocardial infarction, inflammation,
CC tissue ischaemia in the lower extremities, infarction, trauma, vascular
CC occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock,
CC chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia,
CC epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,
CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy
CC with neovascularisation. Suppressing an immune response is useful for
CC ameliorating a symptom of an autoimmune disease such as systemic lupus
CC erythematosus, multiple sclerosis, insulin dependent diabetes mellitus,
CC Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis,
CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
CC anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo,
CC gluten-sensitive enteropathy, autoimmune neuropenia, myasthenia gravis,
CC idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's
CC disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune
CC infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and
CC dense deposit disease. The method is useful in preventing or treating
CC specific proliferative and oncogenic disease which includes sarcomas and
CC carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia,
CC fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency,
CC hypoproliferative disorders, physical trauma, lesions and wounds. The
CC method is also used in gene therapy. The present sequence is human
CC protein related to angiogenesis regulation
XX

SQ Sequence 769 AA;
Query Match 98.7%; Score 1157; DB 5; Length 769;
Best Local Similarity 98.7%; Pred. No. 7.8e-98;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60

Db 130 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189
QY 61 GNNQSVTRQMKQOLEQMLTALDQMRRSIVSELGILLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQMKQOLEQMLTALDQMRRSIVSELGILLSAMEYVQKTLTDEELADWKRQOI 249
QY 121 ACIGGPNICLDRLENNWITSLAESQIQTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 180
Db 250 ACIGGPNICLDRLENNWITSLAESQIQTRQOIKKLELOQKVS YKGDPIVOHRPMLERI 309
QY 181 VELFRNLMSAFVVERQPCWMPHDPRLVIKTVQFTTKVRLVKEPEL 229
Db 310 VELFRNLMSAFVVERQPCWMPHDPRLVIKTVQFTTKVRLVKEPEL 358

RESULT 13

AAR82995
ID AAR82995 standard; protein; 770 AA.
XX
XX AAR82995;
XX
XX 25-MAR-1996 (first entry)
XX
XX Mouse liver acute phase response factor.
XX
XX Mouse; acute phase response factor; transcription factor; interleukin-6;
XX signal transmission; liver; antibody; antisenase; ribozyme;
XX antiinflammatory; antitumor; hypotensive; therapy.
XX
XX Mus musculus.
XX
XX OS
XX
XX EP676469-A2.
XX
XX 11-OCT-1995.
XX
XX 29-MAR-1995; 95BP-00104670.
XX
XX 04-APR-1994; 94JP-00065825.
XX
XX (KISH/) KISHIMOTO T.
XX
XX Akira S, Kishimoto T;
XX WPI; 1995-346089/45.
XX N-PSDB; AAT05619.
XX
XX New acute phase response factor - for developing inhibitory agents for
XX treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory
XX diseases.
XX
XX Claim 10; Page 20-22; 31pp; English.

The sequence represents a mouse acute phase response factor (APRF), a
transcription factor related to signal transmission of interleukin-6 (IL-
6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA
library using a polymerase chain reaction product (amplified using
primers derived from an IL-6-treated mouse liver peptide) as a probe.
APRF-inhibitors, e.g. antibodies, antisense oligonucleotides or
ribozymes, may be used to treat diseases induced by IL-6, e.g.
inflammatory disease, leukemia, cancer, osteoclasia, pulmonary
hypertension, etc

SQ Sequence 770 AA;

Query Match 98.7%; Score 1157; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 7.8e-98;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60

Db 130 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189

QY 61 GNNQSVTRQKMOOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 190 GNNQSVTRQKMOOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRQOI 249
 QY 121 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLELOQKVSYGKDPVVOHRPMLERI 180
 DB 250 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLELOQKVSYGKDPVVOHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPPPEL 229
 DB 310 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPPPEL 358

RESULT 14

AA03768
 ID AAY03768 standard; protein; 770 AA.

XX AC AAY03768;

XX DT 11-JUN-1999 (first entry)

XX DE Human STAT3 allelic variant.

XX KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;
 KW intracellular transcription factor; interleukin-6; medicament; variant;
 KW pharmaceutical; autoimmune disease; inflammatory; human.
 XX OS Homo sapiens.

XX PN EP905234-A2.

XX PD 31-MAR-1999.

XX PF 18-FEB-1998; 98EP-00102774.

XX PR 16-SEP-1997; 97EP-00116061.

XX PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

XX PI Serlupi-Crescenzi O, Della Pietra L;

XX DR WPI; 1999-192664/17.

XX DR N-PSDB; AAX29281.

XX PT New human Signal Transducer and Activator of Transcription 3 (STAT3)

XX PT allelic variant useful for treatment of autoimmune and inflammatory

XX PS disease.

XX PS Claim 2; Page 9-13; 32pp; English.

XX CC The present sequence represents a predominant allelic variant of human
 CC Signal Transducer and Activator of Transcription 3 (STAT3) protein, an
 CC intracellular transcription factor which mediates IL-6 signals. The
 CC encoding sequence differs from the original published human STAT3 gene
 CC sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3
 CC DNA molecule can be used for the recombinant expression of the variant.
 CC STAT3 protein is useful as a medicament or pharmaceutical composition for
 CC treatment of autoimmune or inflammatory diseases
 XX SQ Sequence 770 AA;

Query Match 98.7%; Score 1157; DB 2; Length 770;
 Best Local Similarity 98.7%; Pred. NO. 7.8e-98;
 Matches 256; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 60
 DB 130 NHPTAAVTEKQOMLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRQOI 189

QY 61 GNNQSVTRQKMOOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
 DB 190 GNNQSVTRQKMOOLEQMLTALDQRRSIVSELAGLLSAMEYVQKTLTDEELADWKRQOI 249

QY 121 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLELOQKVSYGKDPVVOHRPMLERI 180
 DB 250 ACIGGPNICLDRLENWITSLAESQLQTRQOIKKLELOQKVSYGKDPVVOHRPMLERI 309
 QY 181 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPPPEL 229
 DB 310 VELFRNLMSAFVVERQPCMPHPDRPLVKTGVQFTTKVRLLVKPPPEL 358

RESULT 15

AA012377

ID AAB12377 standard; peptide; 770 AA.

XX AC AAB12377;

XX DT 08-NOV-2000 (first entry)

XX DE N-terminal domain of murine STAT-3 protein.

XX KW STAT; signal transducer and activator of transcription; crystal;

XX KW drug design; murine.

XX OS Mus sp.

XX FH Key

XX FT Region

XX FT /label= Alpha helix 1

XX FT Region

XX FT /label= Alpha helix 2

XX FT Region

XX FT /label= 3 (10) helix of alpha helix 2

XX FT Region

XX FT /label= Alpha helix 3

XX FT Region

XX FT /label= Alpha helix 4

XX FT Region

XX FT /label= Alpha helix 5

XX FT Region

XX FT /label= Alpha helix 6

XX FT Region

XX FT /label= Alpha helix 7

XX FT Region

XX FT /label= Alpha helix 8

XX FT

XX US6087478-A.

XX PN 11-JUL-2000.

XX PF 23-JAN-1998; 98US-00012710.

XX PR 23-JAN-1998; 98US-00012710.

XX PA (UYRQ) UNIV ROCKEFELLER.

XX PI Vinkemeier U, Moarefi I, Darnell JE, Kuriyan J;

XX DR WPI; 2000-505108/45.

XX PT New crystals of an N-terminal fragment of a signal transducer and

XX PT activator of transcription that effectively diffracts x-rays, useful for

XX PT drug screening and development.

XX PS Disclosure; Fig 1; 42pp; English.

XX CC The present invention relates to a crystal of an N-terminal fragment of a

XX CC signal transducer and activator of transcription (STAT) protein. The

XX CC crystal effectively diffracts X-rays, allowing the determination of the

XX CC atomic coordinates of the N-terminal domain to a resolution of greater

XX CC than 5.0 Angstroms. The present sequence is the N-terminal domain of the

XX CC murine STAT3 protein. The N-terminal domain enables STAT dimers to

XX CC interact and bind DNA cooperatively, a mechanism important for gene

XX CC activation. The crystals are useful in drug screening and development by

XX CC selecting a potential drug by performing rational drug design with the 3-

CC dimensional structure determined for the crystal

XX
SQ Sequence 770 AA;

Query Match 98.7%; Score 1157; DB 3; Length 770;
Best Local Similarity 98.7%; Pred. No. 7.8e-98;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	NHPTAAVTEKQMLEQHLQDARKVQDLQKMKVVENLQDDFDNFYKTLKSGDMQDLN	60
Db	130	NHPTAAVTEKQMLEQHLQDVRKRVQDLQKMKVVENLQDDFDNFYKTLKSGDMQDLN	189
Qy	61	GNNQSVTRQKMQQLEQMLTALDQWRSIVSELAMEYVOKLTDEELADWKRPEI	120
Db	190	GNNQSVTRQKMQQLEQMLTALDQWRSIVSELAMEYVOKLTDEELADWKRQOI	249
Qy	121	ACIGPPNICLDRLNNWITSIAESQLQTRQIKLELQKQSVYKGDPIVQHRPMLERI	180
Db	250	ACIGPPNICLDRLNNWITSIAESQLQTRQIKLELQKQSVYKGDPIVQHRPMLERI	309
Qy	181	VELFRNLKSAFVVERQPCMPMHDPRLVKTGVQFTTKVRLLVKFPPEL	229
Db	310	VELFRNLKSAFVVERQPCMPMHDPRLVKTGVQFTTKVRLLVKFPPEL	358

Search completed: May 25, 2005, 17:36:39
Job time : 123.057 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:25:01 ; Search time 28.6534 Seconds
(without alignments)
596.600 Million cell updates/sec

Title: US-10-090-185-31
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQOMLEQHLLQ.....IKTGVOFTTKVRLLVKFPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1172	100.0	229	3	US-09-387-418A-31
2	1168	99.7	229	3	US-09-387-418A-18
3	1168	99.7	229	3	US-09-387-418A-28
4	1168	99.7	252	3	US-09-387-418A-14
5	1168	99.7	271	3	US-09-387-418A-9
6	1168	99.7	770	1	US-08-369-796-12
7	1168	99.7	770	2	US-08-852-091-12
8	1168	99.7	770	2	US-08-820-754-12
9	1168	99.7	770	3	US-08-956-652-12
10	1168	99.7	770	3	US-08-956-869-12
11	1168	99.7	770	3	US-08-948-547-12
12	1168	99.7	770	3	US-09-364-970-3
13	1168	99.7	770	3	US-09-364-970-5
14	1168	99.7	770	3	US-08-956-653A-12
15	1168	99.7	770	4	US-08-212-185-12
16	1168	99.7	770	5	PCT-US95-17025-12
17	1163	99.2	229	3	US-09-387-418A-30
18	1157	98.7	770	1	US-08-416-581B-9
19	1157	98.7	770	3	US-09-012-710-8
20	1157	98.7	770	3	US-09-556-273-8
21	1157	98.7	770	3	US-09-526-542-2
22	1157	98.7	770	4	US-10-117-087-2
23	1152	98.3	770	1	US-08-416-581B-1
24	1152	98.3	770	1	US-08-416-581B-5
25	1152	98.3	770	3	US-09-087-465-6
26	1152	98.3	770	4	US-09-972-800A-6
27	1152	98.3	771	1	US-08-276-099A-14

28	1152	98.3	771	1	US-08-781-890-14	Sequence 14, Appl
29	1151	98.2	229	3	US-09-387-418A-29	Sequence 29, Appl
30	1090	93.0	213	3	US-09-387-418A-19	Sequence 19, Appl
31	1090	93.0	236	3	US-09-387-418A-15	Sequence 15, Appl
32	1044	89.1	223	3	US-09-387-418A-22	Sequence 22, Appl
33	845	72.1	185	3	US-09-387-418A-23	Sequence 23, Appl
34	777	66.3	176	3	US-09-387-418A-16	Sequence 16, Appl
35	653	55.7	128	3	US-09-387-418A-20	Sequence 20, Appl
36	601	51.3	143	3	US-09-387-418A-17	Sequence 17, Appl
37	571	48.7	129	3	US-09-387-418A-24	Sequence 24, Appl
38	569	48.5	268	4	US-09-387-418A-12	Sequence 12, Appl
39	569	48.5	582	4	US-09-430-806A-3	Sequence 3, Appl
40	569	48.5	712	1	US-08-369-796-6	Sequence 6, Appl
41	569	48.5	712	2	US-08-852-091-6	Sequence 6, Appl
42	569	48.5	712	2	US-08-820-754-6	Sequence 6, Appl
43	569	48.5	712	3	US-08-956-652-6	Sequence 6, Appl
44	569	48.5	712	3	US-08-956-869-6	Sequence 6, Appl
45	569	48.5	712	3	US-08-948-547-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-387-418A-31
; Sequence 31, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/09/387,418A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-387-418A-31

Query Match	100.0%	Score 1172;	DB 3;	Length 229;
Best Local Similarity	100.0%	Pred No. 2.7e-99;	Mismatches 0;	Indels 0; Gaps 0;
Matches 229;	Conservative 0;			
Qy	1	NHPTAAVTEKQOMLEQHLLQDARKRVQDLEQKMVVENLQDDPFDFFNYKTLKSGQDMODLN	60	
Db	1	NHPTAAVTEKQOMLEQHLLQDARKRVQDLEQKMVVENLQDDPFDFFNYKTLKSGQDMODLN	60	
Qy	61	GNNQSVTRQKMQOQLTALQDMRRSIVSELAGLLSMEYVQKTLTDEELADWKRPEI	120	
Db	61	GNNQSVTRQKMQOQLTALQDMRRSIVSELAGLLSMEYVQKTLTDEELADWKRPEI	120	
Qy	121	ACIGGPNICLDRLENIITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI	180	
Db	121	ACIGGPNICLDRLENIITSLAESQLOTRQOIKKLEELQOKVSYKGDPIVQHRPMLERI	180	
Qy	181	VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL	229	
Db	181	VELFRNLMSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL	229	

RESULT 2
US-09-387-418A-18
; Sequence 18, Application US/09387418A
; Patent No. 6391572
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H

Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPDFNYKTLKSQGMQDLN 60
Db 24 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPDFNYKTLKSQGMQDLN 83
QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 84 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143
QY 121 ACIGGPPNICLDLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 180
Db 144 ACIGGPPNICLDLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 203
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGQVQTTKVRLLVKEPEL 229
Db 204 VELFRNLMSAFVVERQPCMPHDPRLVKTGQVQTTKVRLLVKEPEL 252

RESULT 6
US-08-369-796-12
; Sequence 12, Application US/08369796
; Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-369-796-12

Query Match 99.7%; Score 1168; DB 1; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPDFNYKTLKSQGMQDLN 60
Db 130 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPDFNYKTLKSQGMQDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

Db 190 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNICLDLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 180
Db 250 ACIGGPPNICLDLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 309
QY 181 VELFRNLMSAFVVERQPCMPHDPRLVKTGQVQTTKVRLLVKEPEL 229
Db 310 VELFRNLMSAFVVERQPCMPHDPRLVKTGQVQTTKVRLLVKEPEL 358

RESULT 7
US-08-852-091-12
; Sequence 12, Application US/08852091
; Patent No. 5883228
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,091
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/369,796
; FILING DATE: 06-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-852-091-12

Query Match 99.7%; Score 1168; DB 2; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPDFNYKTLKSQGMQDLN 60
Db 130 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPDFNYKTLKSQGMQDLN 189
QY 61 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
QY 121 ACIGGPPNICLDLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 180
Db 250 ACIGGPPNICLDLENWITSLAESQLQTRQIQKLEELQKVSQKGDPIVQHRPMLLEERI 309


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Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NHPTAAVVTKEQWLEQHLQDARKRVQDLEQKMKVVENLODDFDNFYKTLKSQGDMDLN 60
Db 130 NHPTAAVVTKEQWLEQHLQDVRKRVQDLEQKMKVVENLODDFDNFYKTLKSQGDMDLN 189

Qy 61 GNNQSVTRQWQWQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQWQWQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

Qy 121 ACTGGPNICLDRLNWTSLAESOLOTROQIKKLEELQKVSYKGDPIVQHRPMLERI 180
Db 250 ACTGGPNICLDRLNWTSLAESOLOTROQIKKLEELQKVSYKGDPIVQHRPMLERI 309

Qy 181 VELFRNLMSAFVVERPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 229
Db 310 VELFRNLMSAFVVERPCMPMPDRPLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 10
US-08-956-869-i2
; Sequence 12, Application US/08956869
; Patent No. 6030808
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,869
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/212,185
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12

Query Match          99.7%; Score 1168; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189

QY 61 GNNQSVTRQKMQOLEQMLTALDQRRSIVSELAGLISAMEYVQKTLTDEELADWKRPEI 120
DB 190 GNNQSVTRQKMQOLEQMLTALDQRRSIVSELAGLISAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACTGGPPNICLDRLNWNITSLAESQLQTRQOIKKLELQOKVSVYKGDPIVOHRPMLERI 180
DB 250 ACTGGPPNICLDRLNWNITSLAESQLQTRQOIKKLELQOKVSVYKGDPIVOHRPMLERI 309

QY 181 VELFRNLKMSAFVVERPCMPMPDRPLVIKTVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKMSAFVVERPCMPMPDRPLVIKTVQFTTKVRLLVKFPPEL 358

RESULT 11
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-956-869-12

Query Match          99.7%   Score 1168; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98; 1; Indels 0;
Matches 228; Conservative 0; Mismatches 0;

QY 1 NHPTAAVVTBQQMLEQHLQADARKRVQDLEQKMKVVENLQDDFDNFYKTKLKSQQ
DB 130 NHPTAAVVTBQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDNFYKTKLKSQQ
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DB 190 GNGQSVTRQKMQQLEQMLTALDQWRRSIVSELAGLLSAMEYVQKTLTDEELAD
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DB 250 ACTGGPNICLDRLNNWITSLSAQSLOTROQIKLEELQOKVSVYKGDPVVOHRI
QY 181 VELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKFFPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKFFPEL 358

RESULT 11
US-08-948-547-12
; Sequence 12, Application US/08948547
; Patent No. 6124118
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,547
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12

Query Match 99.7%; Score 1168; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDQDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDQDLN 189
QY 61 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 249
QY 121 ACIGGPNICLDRLNNWITSLSAESQLQTRQIKKLEELQKVS YKGGPIVQHRPMLREI 180
DB 250 ACIGGPNICLDRLNNWITSLSAESQLQTRQIKKLEELQKVS YKGGPIVQHRPMLREI 309
QY 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 12
US-09-364-970-3
Sequence 3, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-3

Query Match 99.7%; Score 1168; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDQDLN 60
DB 130 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDQDLN 189
QY 61 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 120
DB 190 GNNQSVTRQKMQOQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRRPEI 249
QY 121 ACIGGPNICLDRLNNWITSLSAESQLQTRQIKKLEELQKVS YKGGPIVQHRPMLREI 180
DB 250 ACIGGPNICLDRLNNWITSLSAESQLQTRQIKKLEELQKVS YKGGPIVQHRPMLREI 309
QY 181 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVIKTGVQFTTKVRLLVKFPPEL 358

RESULT 13
US-09-364-970-5
Sequence 5, Application US/09364970
Patent No. 6235873
GENERAL INFORMATION:
APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
FILE REFERENCE: 600-1-252
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 770
TYPE: PRT
ORGANISM: Mus musculus
US-09-364-970-5

Query Match 99.7%; Score 1168; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGDMDQDLN 60
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QY 121 ACIGGPNICLDRLNNWITSLSAESQLQTRQIKKLEELQKVS YKGGPIVQHRPMLREI 180
DB 250 ACIGGPNICLDRLNNWITSLSAESQLQTRQIKKLEELQKVS YKGGPIVQHRPMLREI 309
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RESULT 14
US-08-956-653A-12
Sequence 12, Application US/08956653A
Patent No. 6338949
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,653A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994


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; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-956-653A-12

Query Match 99.7%; Score 1168; DB 3; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NHPTAAVVVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDPFNYKTLKSQGDMDLN 60
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Qy 61 GNNQSVTRQKMQOLEQMLTALDQWRRSIVSELAGLLSAMEYVQKLTIDELADWKRRPEI 120
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Qy 121 ACTGGPPNI CLDRLENWITS LAESQLOTRQOI KKEELQOKVSVYKGDPIVQHRPMLERI 180
Db 250 ACTGGPPNI CLDRLENWITS LAESQLOTRQOI KKEELQOKVSVYKGDPIVQHRPMLERI 309

Qy 181 VELFRNLKSAFVVERQPCMPMHDPDRPLVITKGQVTTKVRLLVKFPPEL 229
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RESULT 15
US-08-212-185-12
; Sequence 12, Application US/08212185
; Patent No. 6605442
; GENERAL INFORMATION:
; APPLICANT: Darnell Jr., James E.
; APPLICANT: Schindler, Christian W.
; APPLICANT: Fu, Xian-Yuan
; APPLICANT: Wen, Zilong
; APPLICANT: Zhong, Zhong
; TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-212-185--12

Query Match          99.7%; Score 1168; DB 4; Length 770;
Best Local Similarity 99.6%; Pred. No. 3e-98;
Matches 228; Conservative 0; Mismatches 1; Indels 0;

Qy 1 NHPTAAVVTKEQOMLEOHLQADAKRQVODLEQKMKVVENLQDDDFNFYKTLKSKQ
Db 130 NHPTAAVVTKEQOMLEOHLQDVRKRQVODLEQKMKVVENLQDDDFNFYKTLKSKQ

Qy 61 GNNQSVTRQKQOOLEOMLTALDQWRRSIVSELAGLISAMEVQKLTLDDELAAD
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Qy 121 ACIGGGPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVSXKGDPIVQHRR
Db 250 ACIGGGPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVSXKGDPIVQHRR

Qy 181 VELFRNLMSKSAFVVERQPCMPMPHDPRLVITKGQVFTTKVRLLVKPPPEL 229
Db 310 VELFRNLMSKSAFVVERQPCMPMPHDPRLVITKGQVFTTKVRLLVKPPPEL 358

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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763.830 Million cell updates/sec

Title: US-10-090-185-31
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQOMLEQHLQ.....IKTGQFTTKVRLLVKFPPEL 229

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1168	99.7	229	13 US-10-090-185-18	Sequence 18, Appl
3	1168	99.7	229	13 US-10-090-185-28	Sequence 28, Appl
4	1168	99.7	252	13 US-10-090-185-14	Sequence 14, Appl
5	1168	99.7	271	13 US-10-090-185-9	Sequence 9, Appl
6	1168	99.7	770	11 US-09-876-773-12	Sequence 12, Appl
7	1168	99.7	770	17 US-10-639-617-12	Sequence 12, Appl
8	1163	99.2	229	13 US-10-090-185-30	Sequence 30, Appl
9	1157	98.7	720	15 US-10-380-020-4	Sequence 4, Appl
10	1157	98.7	769	15 US-10-380-020-2	Sequence 2, Appl
11	1157	98.7	769	15 US-10-380-020-5	Sequence 5, Appl
12	1157	98.7	770	14 US-10-045-792-8	Sequence 8, Appl
13	1157	98.7	770	14 US-10-038-010-56	Sequence 56, Appl

14	1157	98.7	770	14	US-10-117-087-2	Sequence 2, Appl
15	1157	98.7	793	9	US-09-925-302-780	Sequence 780, App
16	1157	98.7	793	10	US-09-925-302-780	Sequence 780, App
17	1154	98.5	770	15	US-10-116-275-329	Sequence 329, App
18	1152	98.3	770	15	US-10-116-275-349	Sequence 349, App
19	1151	98.2	229	13	US-10-090-185-29	Sequence 29, Appl
20	1090	93.0	213	13	US-10-090-185-19	Sequence 19, Appl
21	1090	93.0	236	13	US-10-090-185-15	Sequence 15, Appl
22	1044	89.1	223	13	US-10-090-185-22	Sequence 22, Appl
23	845	72.1	185	13	US-10-090-185-23	Sequence 23, Appl
24	777	66.3	176	13	US-10-090-185-16	Sequence 16, Appl
25	653	55.7	128	13	US-10-090-185-20	Sequence 20, Appl
26	601	51.3	143	13	US-10-090-185-17	Sequence 17, Appl
27	573	48.9	749	9	US-09-833-205-4	Sequence 4, Appl
28	571	48.7	129	13	US-10-090-185-24	Sequence 24, Appl
29	569	48.5	268	13	US-10-090-185-12	Sequence 12, Appl
30	569	48.5	582	14	US-10-245-120-3	Sequence 3, Appl
31	569	48.5	712	11	US-09-876-773-6	Sequence 6, Appl
32	569	48.5	712	14	US-10-245-120-2	Sequence 2, Appl
33	569	48.5	712	17	US-10-639-617-6	Sequence 6, Appl
34	569	48.5	712	17	US-10-936-390-5	Sequence 5, Appl
35	569	48.5	750	9	US-09-833-205-2	Sequence 2, Appl
36	569	48.5	750	11	US-09-876-773-4	Sequence 4, Appl
37	569	48.5	750	14	US-10-245-120-1	Sequence 1, Appl
38	569	48.5	750	14	US-10-308-279-44	Sequence 44, Appl
39	569	48.5	750	16	US-10-753-889-352	Sequence 352, App
40	569	48.5	750	16	US-10-753-889-823	Sequence 823, App
41	569	48.5	750	17	US-10-492-043-19	Sequence 19, Appl
42	569	48.5	750	17	US-10-639-617-4	Sequence 4, Appl
43	569	48.5	786	9	US-09-925-297-550	Sequence 550, App
44	562	48.0	749	9	US-09-833-205-6	Sequence 6, Appl
45	562	48.0	749	11	US-09-876-773-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-10-090-185-31
; Sequence 31, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 31
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-31

Query Match 100.0%; Score 1172; DB 13; Length 229;
Best Local Similarity 100.0%; Pred. No. 7.5e-95;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NHPTAAVTEKQOMLEQHLQDARKKRVQDLEQKKVVENLQDDFDFFNYKTLKSGQMDQDLN 60
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QY 61 GNNQSVTRKMQOOLEQMLTALDQMRRESIVSELAGLLSAMEYVQKTLTDELDADWKRPEI 120
DB 61 GNNQSVTRKMQOOLEQMLTALDQMRRESIVSELAGLLSAMEYVQKTLTDELDADWKRPEI 120

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QY 121 ACIGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVKVYKGDPIVQHRPMLERI 180
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QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 229
Db 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 229

RESULT 2
US-10-090-185-18
; Sequence 18, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 18
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-18

Query Match 99.7%; Score 1168; DB 13; Length 229;
Best Local Similarity 99.6%; Pred. No. 1.7e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 3
US-10-090-185-28
; Sequence 28, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-28

Query Match 99.7%; Score 1168; DB 13; Length 229;
Best Local Similarity 99.6%; Pred. No. 1.7e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 121 ACIGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVKVYKGDPIVQHRPMLERI 180
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Db 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 229

RESULT 4
US-10-090-185-14
; Sequence 14, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14

Query Match 99.7%; Score 1168; DB 13; Length 252;
Best Local Similarity 99.6%; Pred. No. 1.9e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 GNNQSVTRQMKQOMLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
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US-10-090-185-9

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; LENGTH: 229
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-28

Query Match 99.7%; Score 1168; DB 13; Length 229;
Best Local Similarity 99.6%; Pred. No. 1.7e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLODDFDFNYKTLKSGDMQDLN 60
Db 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLODDFDFNYKTLKSGDMQDLN 60
QY 61 GNNQSVTRQMKQOMLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 61 GNNQSVTRQMKQOMLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
QY 121 ACIGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVKVYKGDPIVQHRPMLERI 180
Db 121 ACIGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVKVYKGDPIVQHRPMLERI 180
QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 229
Db 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 229

RESULT 4
US-10-090-185-14
; Sequence 14, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wzesczynska, Melissa H
; APPLICANT: Horvath, Curt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; TITLE OF INVENTION: INTERACTIONS
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/387,418
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-14

Query Match 99.7%; Score 1168; DB 13; Length 252;
Best Local Similarity 99.6%; Pred. No. 1.9e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLODDFDFNYKTLKSGDMQDLN 60
Db 24 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLODDFDFNYKTLKSGDMQDLN 83
QY 61 GNNQSVTRQMKQOMLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 84 GNNQSVTRQMKQOMLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 143
QY 121 ACIGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVKVYKGDPIVQHRPMLERI 180
Db 144 ACIGPPNICLDRLNWIITSLAESQLOTRQOIKKLELOQKVKVYKGDPIVQHRPMLERI 203
QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 229
Db 204 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 252

RESULT 5
US-10-090-185-9

```

Sequence 9, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
PRIOR FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 271
TYPE: PRT
ORGANISM: Mus musculus
US-10-090-185-9

Query Match 99.7%; Score 1168; DB 13; Length 271;
Best Local Similarity 99.6%; Pred. No. 2,1e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
Db 24 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 83
QY 61 GNNQSVTRQKMOQLQMLTALDOMRSIVSELQKMLVVENLQDDPFDNFYKTLKSQGMQDLN 120
Db 84 GNNQSVTRQKMOQLQMLTALDOMRSIVSELQKMLVVENLQDDPFDNFYKTLKSQGMQDLN 143
QY 121 ACIGGPPNICLDRLENWITSLSAQSLOTRQKQIKLEELQKMLVVENLQDDPFDNFYKTLKSQGMQDLN 180
Db 144 ACIGGPPNICLDRLENWITSLSAQSLOTRQKQIKLEELQKMLVVENLQDDPFDNFYKTLKSQGMQDLN 203
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVTKTGVQFTTKVRLLVKPEL 229
Db 204 VELFRNLKMSAFVVERQPCMPHDPRLVTKTGVQFTTKVRLLVKPEL 252

RESULT 6
US-09-876-773-12
Sequence 12, Application US/09876773
Publication No. US20040058318A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,773
FILING DATE: 07-Jun-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-876-773-12

Query Match 99.7%; Score 1168; DB 11; Length 770;
Best Local Similarity 99.6%; Pred. No. 7.9e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 60
Db 130 NHPTAAVTEKQMLEQHLQDARKRVQDLEQKMKVVENLQDDPFDNFYKTLKSQGMQDLN 189
QY 61 GNNQSVTRQKMOQLQMLTALDOMRSIVSELQKMLVVENLQDDPFDNFYKTLKSQGMQDLN 120
Db 190 GNNQSVTRQKMOQLQMLTALDOMRSIVSELQKMLVVENLQDDPFDNFYKTLKSQGMQDLN 249
QY 121 ACIGGPPNICLDRLENWITSLSAQSLOTRQKQIKLEELQKMLVVENLQDDPFDNFYKTLKSQGMQDLN 180
Db 250 ACIGGPPNICLDRLENWITSLSAQSLOTRQKQIKLEELQKMLVVENLQDDPFDNFYKTLKSQGMQDLN 309
QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVTKTGVQFTTKVRLLVKPEL 229
Db 310 VELFRNLKMSAFVVERQPCMPHDPRLVTKTGVQFTTKVRLLVKPEL 358

RESULT 7
US-10-639-617-12
Sequence 12, Application US/10639617
Publication No. US20050079543A1
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
Schindler, Christian W.
Fu, Xian-Yuan
Wen, Zilong
Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/639,617
; FILING DATE: 12-AUG-2003
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,185
; FILING DATE: 11-MAR-1994
; APPLICATION NUMBER: US 07/980,498
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: US 07/854,296
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: WO US93/02569
; FILING DATE: 19-MAR-1993
; APPLICATION NUMBER: US 08/126,588
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-073 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 139521
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-639-617-12

Query Match 99.7%; Score 1168; DB 17; Length 770;
Best Local Similarity 99.6%; Pred. No. 7.9e-94;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 189

QY 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPEL 229
Db 310 VELFRNLMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPEL 358

RESULT 8
US-10-090-185-30
; Sequence 30, Application US/10090185
; Publication No. US20020197647A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Xiaokui
; APPLICANT: Wrzeszczynska, Melissa H
; APPLICANT: Horvath, Kurt M
; APPLICANT: Darnell Jr., James E
; TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
; FILE REFERENCE: 600-1-253
; CURRENT APPLICATION NUMBER: US/10/090,185
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 229

;
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-090-185-30

Query Match 99.2%; Score 1163; DB 13; Length 229;
Best Local Similarity 99.1%; Pred. No. 4.6e-94;
Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 60
Db 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 60

QY 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120

QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 180
Db 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 180

QY 181 VELFRNLMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPEL 229
Db 181 VELFRNLMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPEL 229

RESULT 9
US-10-380-020-4
; Sequence 4, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-020-4

Query Match 98.7%; Score 1157; DB 15; Length 720;
Best Local Similarity 98.7%; Pred. No. 6.7e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSQGMQDLN 189

QY 61 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 120
Db 190 GNNQSVTRQKMQOLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249

QY 121 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 180
Db 250 ACIGGPPNICLDRLNWIITSLAESQLQTRQIQKLEELQKVS YKGDPIVQHRPMLERI 309

QY 181 VELFRNLMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPEL 229
Db 310 VELFRNLMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPEL 358

RESULT 10
US-10-380-020-2
; Sequence 2, Application US/10380020
; Publication No. US20040052762A1

```
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 769
; TYPE: PRT<
; ORGANISM: Homo Sapiens
; ORGANISM: Homo Sapiens
US-10-380-020-2

Query Match          98.7%; Score 1157; DB 15; Length 769;
Best Local Similarity 98.7%; Pred. No. 7.3e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 60
      |||
Db      130 NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 189
      |||

QY      61  GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQI 120
      |||
Db      190 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQI 249
      |||

QY      121 ACIGPPNICLDRLENWITSLSAESQLQTRQIIKKLEELQKQVSYKGDPIVQHRPMLERI 180
      |||
Db      250 ACIGPPNICLDRLENWITSLSAESQLQTRQIIKKLEELQKQVSYKGDPIVQHRPMLERI 309
      |||

QY      181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 229
      |||
Db      310 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 358
      |||

RESULT 11
US-10-380-020-5
; Sequence 5, Application US/10380020
; Publication No. US20040052762A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Hua
; APPLICANT: Pardoll, Drew
; APPLICANT: Jove, Richard
; APPLICANT: Dalton, William
; TITLE OF INVENTION: Stat3 Agonists and Antagonists and Therapeutic Uses Thereof
; FILE REFERENCE: 10873-009-999
; CURRENT APPLICATION NUMBER: US/10/380,020
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/231,212
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Homo Sapiens
; ORGANISM: Homo Sapiens
US-10-380-020-5

Query Match          98.7%; Score 1157; DB 15; Length 769;
Best Local Similarity 98.7%; Pred. No. 7.3e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 60
      |||
Db      130 NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 189
      |||

QY      61  GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
      |||
Db      190 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 249
      |||

QY      121 ACIGPPNICLDRLENWITSLSAESQLQTRQIIKKLEELQKQVSYKGDPIVQHRPMLERI 180
      |||
Db      250 ACIGPPNICLDRLENWITSLSAESQLQTRQIIKKLEELQKQVSYKGDPIVQHRPMLERI 309
      |||

QY      181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 229
      |||
Db      310 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 358
      |||
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Db      190 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQI 249
      |||

QY      121 ACIGPPNICLDRLENWITSLSAESQLQTRQIIKKLEELQKQVSYKGDPIVQHRPMLERI 180
      |||
Db      250 ACIGPPNICLDRLENWITSLSAESQLQTRQIIKKLEELQKQVSYKGDPIVQHRPMLERI 309
      |||

QY      181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 229
      |||
Db      310 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 358
      |||

RESULT 12
US-10-045-792-8
; Sequence 8, Application US/10045792
; Publication No. US20030003563A1
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/045,792
; FILING DATE: 19-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-045-792-8

Query Match          98.7%; Score 1157; DB 14; Length 770;
Best Local Similarity 98.7%; Pred. No. 7.3e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 60
      |||
Db      130 NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNFYKTLKSQGMQDLN 189
      |||

QY      61  GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEI 120
      |||
Db      190 GNNQSVTRQKMOQLEQMLTALDOMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQI 249
      |||
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121	QY	ACIGGGPNICLDRLNNWITSLSA	SO	QTRQOI	KKLEELQOKSVYKGDPIVOHPRM	LEERI	180
250	DB	ACIGGGPNICLDRLNNWITSLSA	SO	QTRQOI	KKLEELQOKSVYKGDPIVOHPRM	LEERI	309
181	QY	VELFNLMKSAFVVERQPCMPH	MDRPLVI	KTGVQFTTKVRL	LVAKPPEL	229	
310	DB	VELFNLMKSAFVVERQPCMPH	MDRPLVI	KTGVQFTTKVRL	LVAKPPEL	358	

RESULT 13

```

US-10-038-010-56
; Sequence 56, Application US/10038010
; Publication NO. US20030040089A1 .
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: PIERRE, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: STAT3 : Transcription factor
; LOCATION: (1)..(770)
; OTHER INFORMATION:
US-10-038-010-56

```

Query Match	98.7%;	Score 1157;	DB 14;	Length 770;
Best Local Similarity	98.7%;	Pred. No. 7.3e-93;		
Matches 226;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	NHPTAAVVTEKQWLEQHLQDARKRVQDLREQKMKVVENLQDDPFNFKTLKSQGDMDLN	60	
Db	130	NHPTAAVVTEKQWLEQHLQDVRKRVQDLREQKMKVVENLQDDPFNFKTLKSQGDMDLN	189	
QY	61	GNNQSVTRQKMQQLEQMLTALDQWRRISIVSELAGLLSAMEYVQKTLTDEELADWKRPEI	120	
Db	190	GNNQSVTRQKMQQLEQMLTALDQWRRISIVSELAGLLSAMEYVQKTLTDEELADWKRQOI	249	
QY	121	ACTIGGPPNICLDRLNWIITSLASQLOTRQOIKKLEELQOKVSYKGGPPIVQHRPMLERI	180	
Db	250	ACTIGGPPNICLDRLNWIITSLASQLOTRQOIKKLEELQOKVSYKGGPPIVQHRPMLERI	309	
QY	181	VELFRNLKMSAFVVERQPCMPMPDRLVKTGVQFTTKVRLLVKFPPEL	229	
Db	310	VELFRNLKMSAFVVERQPCMPMPDRLVKTGVQFTTKVRLLVKFPPEL	358	

RESIT.T 14

```

US-10-117-087-2
; Sequence 2, Application US/10117087
; Publication No. US200301668541
; GENERAL INFORMATION:
; APPLICANT: SERLUPI-CRESCENZI, Ottaviano
; APPLICANT: DELLA PIETRA, Linda
; TITLE OF INVENTION: ALLELIC VARIANTS OF HUMAN STAT3
; FILE REFERENCE: SERLUPI=2
; CURRENT APPLICATION NUMBER: US/10/117,087
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/526,542
; PRIOR FILING DATE: 2000-03-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT

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```

; ORGANISM: Human
US-10-117-087-2

Query Match          98.7%; Score 1157; DB 14; Length 770;
Best Local Similarity 98.7%; Pred. No. 7.3e-93;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVVTKEQOMLEQHLODARKRVODLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 60
Db 130 NHPTAAVVTKEQOMLEQHLODVRKRVODLEQKMKVVENLQDDDFNYKTLKSGQDMQDLN 189

QY 61 GNNQSVTRQKMQOOLEWMLTALDQMRSSIVSELAGLISAMEYVQKTLTDESLADWKRPPEI 120
Db 190 GNNQSVTRQKMQOOLEWMLTALDQMRSSIVSELAGLISAMEYVQKTLTDESLADWKRRQOI 249

QY 121 AC1GGPPNICLDRELNWITSLSBSQLOTRQOIKKLEELOOKVSKYKGDPIVQHRPMLLEERI 180
Db 250 AC1GGPPNICLDRELNWITSLSBSQLOTRQOIKKLEELOOKVSKYKGDPIVQHRPMLLEERI 309

QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPPPEL 229
Db 310 VELFRNLMSAFVVERQPCMPMPDRPLVIKTGVQFTTKVRLLVKPPPEL 358

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RESIT.T 15

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US-09-925-302-780
; Sequence 780, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 780
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-780

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	Query Match	98.7%;	Score 1157;	DB 9;	Length 793;
	Best Local Similarity	98.7%;	Pred. No. 7.6e-93;		
	Matches 226;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	NHPTAAVVTKEQOMLEBOHLQDARKRVQDLEEQKMKVVENLQDDDFNYKTKLSQGDMDLN	60		
Db	153	NHPTAAVVTKEQOMLEBOHLQDVRKRVQDLEEQKMKVVENLQDDDFNYKTKLSQGDMDLN	212		
Qy	61	GNNQSVTRQKMOQLEQMLTALDQMRSSIVSELAGLLSAMEYVOKTITDEELADWKRRPEI	120		
Db	213	GNNQSVTRQKMOQLEQMLTALDQMRSSIVSELAGLLSAMEYVOKTITDEELADWKRRQOI	272		
Qy	121	AC1GGPNPNCILDRLENNWTSLSAQLOTRQOIKKLEELQOKVSKGDP1VOHRPMLERI	180		
Db	273	AC1GGPNPNCILDRLENNWTSLSAQLOTRQOIKKLEELQOKVSKGDP1VOHRPMLERI	332		
Qy	181	VELFRNLMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPPPEL	229		
Db	333	VELFRNLMSAFVVERQPCMPMPHDPRLVIKTGVQFTTKVRLLVKPPPEL	381		

Search completed: May 25, 2005, 18:21:55
Job time : 101.62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:24:07 ; Search time 21.6038 Seconds
(without alignments)
1019.898 Million cell updates/sec

Title: US-10-090-185-31
Perfect score: 1172
Sequence: 1 NHPTAAVTEKQOMLEQHLQ.....IKTGQVFTKVRLLVKRPPEL 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1157	98.7	770	2 I49508	ISGF3 p91-related
2	1152	98.3	770	2 A54444	DNA-binding protei
3	523.5	44.7	739	2 A46159	interferon-depende
4	508	43.3	748	2 A56047	gamma-interferon a
5	322	27.5	851	2 A46160	interferon alpha-i
6	268.5	22.9	786	2 I49274	mammary gland fact
7	268.5	22.9	793	2 S54772	mammary gland fact
8	262.5	22.4	794	2 G02317	transcription acti
9	237	20.2	794	2 S55527	mammary gland fact
10	127	10.8	848	2 A54740	interleukin-4-indu
11	125.5	10.7	837	2 I57557	DNA-Binding Protei
12	122.5	10.5	1208	2 AE1947	chromosome segrega
13	122	10.4	533	2 G72593	hypothetical prote
14	122	10.4	978	2 A70387	conserved hypothet
15	120.5	10.3	1166	2 T27075	hypothetical prote
16	116.5	9.9	1509	1 A27224	myosin heavy chain
17	116.5	9.9	2094	2 S33124	tpy protein - huma
18	114.5	9.8	284	2 C64527	M protein - Helico
19	114.5	9.8	857	2 S33821	median body protei
20	113.5	9.7	924	2 S06117	myosin heavy chain
21	113	9.6	1999	1 S21801	myosin heavy chain
22	112.5	9.6	1690	2 T13030	microtubule bindin
23	112.5	9.6	2007	1 B43402	myosin heavy chain
24	112.5	9.6	2253	2 T30336	nuclear/mitotic ap
25	112	9.6	289	2 S51193	epimorphin - mouse
26	112	9.6	1976	2 A59252	myosin heavy chain
27	111	9.5	284	2 S24401	tropomyosin 2, ske
28	111	9.5	734	2 T27055	hypothetical prote
29	111	9.5	853	2 T51505	hypothetical prote

30	111	9.5	1164	2 T24806	hypothetical prote
31	111	9.5	1188	2 G83960	chromosome segrega
32	110.5	9.4	1738	2 T14867	interaptin - slime
33	109.5	9.3	434	2 T43448	hypothetical prote
34	109.5	9.3	464	2 H90279	microtubule bindin
35	109.5	9.3	727	2 AC1814	hypothetical prote
36	109.5	9.3	1048	1 BVSCSC	exonuclease (EC 3.
37	109.5	9.3	1957	2 T38077	hypothetical coile
38	109.5	9.3	2442	2 T08621	centrosome associa
39	109	9.3	1959	1 A33977	myosin heavy chain
40	109	9.3	3187	2 JCS837	364K Golgi complex
41	108.5	9.3	946	2 S28061	SCP1 protein - rat
42	108.5	9.3	1940	2 A52887	myosin heavy chain
43	108.5	9.3	1992	2 A47297	myosin heavy chain
44	108	9.2	2677	2 A38194	desmoplakin 1 - hu
45	107.5	9.2	527	2 S33068	myosin heavy chain

ALIGNMENTS

RESULT 1

I49508
ISGF3 p91-related transcription factor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49508; I49009
R:Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Su
Cell 77, 63-71, 1994
A:Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tr
A:Reference number: A54444; MUID:94208062; PMID:7512451
A:Accession: I49508
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-770 <RES>
A:Cross-references: UNIPROT:P42227; GB:I29278; NID:9476715; PIDN:AAA37254.1; PID:947671
R:Kaz, R.; Durbin, J.E.; Levy, D.E.
J. Biol. Chem. 269, 24391-24395, 1994
A:Title: Acute phase response factor and additional members of the interferon-stimulate
A:Reference number: I49009; MUID:95014185; PMID:7523373
A:Accession: I49009
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-393, 'M', 395-700, 702-770 <RE2>
A:Cross-references: EMBL:U08378; NID:9473889; PIDN:AAA56668.1; PID:9473890
C:Genetics:
A:Gene: APRE
C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 98.7%; Score 1157; DB 2; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.7e-69;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	NHPTAAVTEKQOMLEQHLQDARKVQDLQSKVVENLQDDPDNFKTLKSGQMDLN	60
Db	130	NHPTAAVTEKQOMLEQHLQDVRKRVQDLQSKVVENLQDDPDNFKTLKSGQMDLN	189
Qy	61	GNQSVTRQKMOQLTALDQMRSSIVSELAGLLSAMEYVQKTLTDELDWKRPEI	120
Db	190	GNQSVTRQKMOQLTALDQMRSSIVSELAGLLSAMEYVQKTLTDELDWKRQOI	249
Qy	121	ACIGPPNICLDRLNWTSLAESQLQTRQIQIKLELQKQSVYKGDPIVQHRPMLERI	180
Db	250	ACIGPPNICLDRLNWTSLAESQLQTRQIQIKLELQKQSVYKGDPIVQHRPMLERI	309
Qy	181	VELFRLNPKSAFVVERQCPMPHDPRLVIKTGVQFTTKVRLLVKPEL	229
Db	310	VELFRLNPKSAFVVERQCPMPHDPRLVIKTGVQFTTKVRLLVKPEL	358

RESULT 2
A54444
DNA-binding protein APRF - human

C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: A54444
R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud
Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tra
A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: A54444
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-770 <RES>
A;Cross-references: UNIPROT:P40763; GB:L29277; NID:g475788; PID:g475789
C;Genetics:
A;Gene: GDB:STAT3; APRF
A;Cross-references: GDB:358950
A;Map position: 17q21-17q21
A;Title: A novel gamma interferon activation site-binding protein expressed in e
A;Reference number: A56047; MUID:94277038; PMID:8007943
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription factor

Query Match 98.3%; Score 1152; DB 2; Length 770;
Best Local Similarity 98.3%; Pred. No. 5.9e-69;
Matches 225; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 60
DB 130 NHPTAAVTEKQMLEQHLQDVRKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLN 189

QY 61 GNNQSVTRQKQMLEQMLTALDQMRSSIVSELAGLLSAMEYVQKTLTDESLADWKRPEI 120
DB 190 GNNQSVTRQKQMLEQMLTALDQMRSSIVSELAGLLSAMEYVQKTLTDESLADWKRQOI 249

QY 121 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELOQKVSXKGGPIVQHRPMLERI 180
DB 250 ACIGGPNICLDRLNWTSLAESQLTROQIKKLELHQKVSXKGGPIVQHRPMLERI 309

QY 181 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 VELFRNLKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 358

RESULT 3
A46159
interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46159
R;Schindler, C.; Fu, X.Y.; Imbrota, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG
A;Reference number: A46159; MUID:92366557; PMID:1502203
A;Accession: A46159
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues: 1-739 <SCH>
A;Cross-references: UNIPROT:P42224
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 44.7%; Score 523.5; DB 2; Length 739;
Best Local Similarity 45.8%; Pred. No. 2.6e-27;
Matches 103; Conservative 49; Mismatches 60; Indels 13; Gaps 2;

QY 5 AAVTEKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGDMDLNGNQ 64
DB 132 STVMDLQKELDSKVRNVKQKMCIEHIKSLDQYDFKCTL--QREHETNGVAK 189

QY 65 SVTRQKQMLEQMLTALDQMRSSIVSELAGLLSAMEYVQKTLTDESLADWKRPEIACIG 124
DB 190 SDQKQELLLKMYLMDNKRKEVWHKIIELLNVTELTQNALINDELVEKRRQSQACIG 249

QY 125 GPNICLDRLNWTSLAESQLTROQIKKLELOQKVSXKGGPIVQHRPMLERIVELF 184
DB 250 GPNICLDRLNWTSLAESQLTROQIKKLELHQKVSXKGGPIVQHRPMLERIVELF 309

DB 250 GPNACLDLQ-----QVRQQLKLELEQKYTVEHDPITKNQKQVLWDRTFSLF 298

QY 185 RNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 299 QQLIOSSFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKQEL 343

RESULT 4
A56047
gamma-interferon activation site-binding protein Stat4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56047
R;Yamamoto, K.; Quelle, F.W.; Thierfelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins,
Mol. Cell. Biol. 14, 4342-4349, 1994
A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in e
A;Reference number: A56047; MUID:94277038; PMID:8007943
A;Accession: A56047
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-748 <YAM>
A;Cross-references: UNIPROT:P42228; GB:U09351; NID:g509502; PID:AAA19692.1; PID:g50950
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; phosphoprotein

Query Match 43.3%; Score 508; DB 2; Length 748;
Best Local Similarity 45.5%; Pred. No. 2.8e-26;
Matches 102; Conservative 48; Mismatches 66; Indels 8; Gaps 2;

QY 8 VTEKQMLEQHLQDARKRVQDLQKMKVVENLQDDFDNFYKTLKS--QGDMDLNGNQS 65
DB 136 VSEQRNVHEKVSIAKNSVQMTQDTPKYLELDQDFDYKTIQTMDQGD-----KNSI 189

QY 66 VTRQKQMLEQMLTALDQMRSSIVSELAGLLSAMEYVQKTLTDESLADWKRPEIACIG 125
DB 190 LVNQEVLTQELMNSLDFKKEALSQVITVNETDLLMNSMLEELQDWKRRQOIACIG 249

QY 126 PPNICLDRLNWTSLAESQLTROQIKKLELOQKVSXKGGPIVQHRPMLERIVELF 185
DB 250 PLHGLDQLQNCFTLLAESLFQLRQOLEKQOSTWYEGDPIPAQRAHLLETRATFLY 309

QY 186 NLMKSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 229
DB 310 NLFKNSFVVERQPCMPHDPRLVKTGVQFTTKVRLLVKFPPEL 353

RESULT 5
A46160
interferon alpha-induced transcription activator ISGF-3, 113K chain - human
N;Alternate names: stat2 protein
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46160; S71908; S53873
R;Fu, X.Y.; Schindler, C.; Imbrota, T.; Aebersold, R.; Darnell Jr., J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
A;Title: The proteins of ISGF-3, the interferon alpha-induced transcriptional activator
A;Reference number: A46160; MUID:92366558; PMID:1502204
A;Accession: A46160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-851 <FU>
A;Cross-references: UNIPROT:P52630
A;Note: sequence extracted from NCBI backbone (NCBIP:110820)
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell, J.E.
submitted to the EMBL Data Library, December 1994
A;Reference number: S71908
A;Accession: S71908
A;Molecule type: DNA
A;Residues: 1-851 <YAN>
A;Cross-references: EMBL:U18671; NID:g1293919; PID:AAA98760.1; PID:g1293920
R;Yan, R.; Qureshi, S.; Zhong, Z.; Wen, Z.; Darnell Jr., J.E.
Nucleic Acids Res. 23, 459-463, 1995
A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in

A:Reference number: S53873; MUID:95192056; PMID:7885841

A:Accession: S53873

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-196;392-591;684-730 <YAW>

A:Cross-references: EMBL:U18671

C:Genetics:

A:Gene: stat2

A:Introns: 44/2; 95/3; 127/3; 157/3; 183/1; 211/3; 261/2; 314/2; 345/2; 372/2; 40/2

C:Superfamily: human signal transducer and transcription activator STAT5A

C:Keywords: signal transduction; transcription regulation

Query Match 27.5%; Score 322; DB 2; Length 851;

Best Local Similarity 33.5%; Pred. No. 6.9e-14;

Matches 74; Conservative 51; Mismatches 90; Indels 6; Gaps 4;

QY 8 VTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNYKTLKSGQDMQDLNGNQSVT 67

DB 138 VESQHEIESRILDLRAMKEKLVKISQLKDQDVCFRYK-IOAKGKTPSLDPH--QTK 194

QY 68 RQKMOOLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWKRPEIACIGGPP 127

DB 195 EQKI--LQETNELDKRRKEVLDAKALLGLRTLTIELLL-PKLEWKAQQQKACIRAPI 251

QY 128 NICLDLENWITSLABSQTRQOIKKLELOQKVSQKDPVQHRPMLERIVELFRNL 187

DB 252 DHGLEQLEWTFAGAKLPHLRQLLKLGLSLVSYDDPLTKGVDLRLNAQVTELLQRL 311

QY 188 MKSAFVVERQPCMPHDPRLVKTGVQVFTTKVRLIAVKPE 228

DB 312 LHRAFVETQPCMPQTPHRLIKTGSKFTVTRLLVRLQE 352

RESULT 6

I49274

mammary gland factor - mouse

N:Alternate names: STAT5 protein homolog p80

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49274; S54773; S54727

R:Liou, X.; Robinson, G.W.; Guilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A:Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved in

A:Reference number: I49273; MUID:96004632; PMID:7568026

A:Accession: I49274

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-786 <RES>

A:Cross-references: UNIPROT:P42232; UNIPROT:Q9JUKM1; EMBL:U21110; NID:g747973; PIDN:AA052

R:Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A:Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A:Reference number: S54772; MUID:95237198; PMID:7720707

A:Accession: S54773

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-432,'E',434-786 <MUI>

A:Cross-references: EMBL:248539; NID:g758635; PIDN:CAA8420.1; PID:g758636

R:Azam, M.; Erdjument-Bronage, H.; Kreider, B.L.; Xia, M.; Quelle, F.; Basu, R.; Saris,

EMBO J. 14, 1402-1411, 1995

A:Title: Interleukin-3 signals through multiple isoforms of Stat5.

A:Reference number: S54725; MUID:95246733; PMID:7537213

A:Accession: S54727

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-432,'E',434-786 <AZA>

C:Genetics:

A:Gene: Stat5b

C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.9%; Score 268.5; DB 2; Length 786;

Best Local Similarity 30.6%; Pred. No. 2.2e-10;

Matches 71; Conservative 41; Mismatches 99; Indels 21; Gaps 5;

QY 5 AAVVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNY-KTLKSGQDMQDLNGNN 63

DB 134 ADAMSQKHLQINQTFEELRLITQDTENELKQLQQTQVEFIIOQESLRIOAQPAQLGQLN 193

QY 64 -----QSVTRQKMQQLEQML-----TALDQMRRSIVSELAGLSAMEYVQKTLTDEELA 112

DB 194 PQRMSRETALQKQVSLQVSTLQREAOQLQQRVRLAEKHQKTLQLLRKQQTILDDLELI 253

QY 113 DWKRPEIACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHR 172

DB 254 QMKRRQQLAGNGGPPGSLDLVQSWCEKLAETIWNQROIIRAEHLCCQQLPIPG-PVEEM 312

QY 173 RQMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQVFTTKVRLVV 224

DB 313 LAENVATITDIISALVTSTFIIIEKQP-----POVLKTQTKFAATVRLVV 356

RESULT 7

S54772

mammary gland factor - mouse

N:Alternate names: stat5 protein

C:Species: Mus musculus (house mouse)

C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S54772; I49273

R:Mui, A.L.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A:Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin

A:Reference number: S54772; MUID:95237198; PMID:7720707

A:Accession: S54772

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-793 <MUI>

A:Cross-references: UNIPROT:P42230; UNIPROT:Q9JIAO; EMBL:248538; NID:g758633; PIDN:CAA8

R:Liou, X.; Robinson, G.W.; Guilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A:Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved

A:Reference number: I49273; MUID:96004632; PMID:7568026

A:Accession: I49273

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-793 <RES>

A:Cross-references: EMBL:U21103; NID:g747971; PIDN:AAA80590.1; PID:g747972

C:Genetics:

A:Gene: Stat5a

C:Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.9%; Score 268.5; DB 2; Length 793;

Best Local Similarity 30.6%; Pred. No. 2.2e-10;

Matches 70; Conservative 41; Mismatches 97; Indels 21; Gaps 5;

QY 8 VTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDDFNY-KTLKSGQDMQDLNGNN--- 63

DB 137 MSQKHLQINQRFEEELRLITQDTENELKQLQQTQVEFIIOQESLRIOAQPAQLGQLNPOE 196

QY 64 -----QSVTRQKMQQLEQML-----TALDQMRRSIVSELAGLSAMEYVQKTLTDEELADWK 115

DB 197 RMSRETALQKQVSLQVSTLQREAOQLQQRVRLAEKHQKTLQLLRKQQTILDDLELIQWK 256

QY 116 RPPEIACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQKQVSYKGDPIVQHRPM 175

DB 257 RRQQLAGNGGPPGSLDLVQSWCEKLAETIWNQROIIRAEHLCCQQLPIPG-PVEEMLA 315

QY 176 LEERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQVFTTKVRLVV 224

DB 316 VNATITDIISALVTSTFIIIEKQP-----POVLKTQTKFAATVRLVV 356

RESULT 8

G02317

transcription activator stat5a - human

C:Species: Homo sapiens (man)

C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C;Accession: G02317
R;Lin, J.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:gl151169; PIDN:AA06589.1; PID:gl119
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.4%; Score 262.5; DB 2; Length 794;
Best Local Similarity 30.1%; Pred. No. 5.6e-10;
Matches 69; Conservative 42; Mismatches 97; Indels 21; Gaps 5;

QY 8 VTEKQMLEQLQDARKRVQDLQKMKVVENLQDDFDNY-KTLKSGQMDL----- 59
Db 137 MSQKHLQINQTFEELRLVTDTELKQLOQTQYFIQYQESLRIOAQAQLAQLSPQE 196
QY 60 NGNQSVTRQKMQQLEQML-----TALDQMRSSIVSELAGLLSAMEYVQKTLTDEELADWK 115
Db 197 RLSRETALQKQVSLQVLEAQLQYRVLEAKHKTQLLRKQQTILDELQIOWK 256
QY 116 RRPETACIGGPNICLDRLNWTSLAESQLQTRQKIKLEELQKQVSYKGDPIVQHRPM 175
Db 257 RROQLAGNGPPGSLDVLQSWCEKLAETIWNQRQIRRAEHLCCQLPIPG-PVEEMLA 315
QY 176 LEEBIVELFRLNLMKSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLIV 224
Db 316 VNATITDIISALVTSTFIEIKQP-----PQVLKTQTKFAATVRLIV 356

RESULT 9
S5527
mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S5527; S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regula
A;Reference number: S5527; MUID:9518889; PMID:7862987
A;Accession: S5527
A;Molecule type: mRNA
A;Residues: 1-794 <WAK>
A;Cross-references: UNIPROT:P42231; EMBL:X78428; NID:9602354; PIDN:CAA55191.1; PID:g6023
A;Note: this is a revision to the sequence from reference S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 13, 2182-2191, 1994
A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcri
A;Reference number: S44353; MUID:94244619; PMID:7514531
A;Accession: S44353
A;Molecule type: mRNA
A;Residues: 1-716, 'RHLHGSLPSR', 729, 'P', 731, 'ASL' <WAK>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S5527
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 20.2%; Score 237; DB 2; Length 794;
Best Local Similarity 29.3%; Pred. No. 2.8e-08;
Matches 67; Conservative 41; Mismatches 99; Indels 22; Gaps 6;

QY 8 VTEKQMLEQLQDARKRVQDLQKMKVVENLQDDFDNY-KTLKSGQMDLNGN--- 63
Db 138 MSQKHLQINQTFEELRLVTDTELKQLOQTQYFIQYQESLRIOAQAQLAQLPQE 197
QY 64 ----QSVTRQKMQQLEQML-----TALDQMRSSIVSELAGLLSAMEYVQKTLTDEELADWK 115
Db 198 RLSRETALQKQVSLQVLEAQLQYRVLEAKHKTQLLRKQQTILDELQIOWK 257
QY 116 RRPETACIGGPNICLDRLNWTSLAESQLQTRQKIKLEELQKQVSYKGDPIVQHRPM 175
Db 258 RRDWRGWEAPPR-SLDVLQSWCEKLAETIWNQRQIRRAEHLCCQLPIPG-PVEEMLA 315

C;Accession: G02317
R;Lin, J.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-794 <LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:gl151169; PIDN:AA06589.1; PID:gl119
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 22.4%; Score 262.5; DB 2; Length 794;
Best Local Similarity 30.1%; Pred. No. 5.6e-10;
Matches 69; Conservative 42; Mismatches 97; Indels 21; Gaps 5;

QY 8 VTEKQMLEQLQDARKRVQDLQKMKVVENLQDDFDNY-KTLKSGQMDL----- 59
Db 137 MSQKHLQINQTFEELRLVTDTELKQLOQTQYFIQYQESLRIOAQAQLAQLSPQE 196
QY 60 NGNQSVTRQKMQQLEQML-----TALDQMRSSIVSELAGLLSAMEYVQKTLTDEELADWK 115
Db 197 RLSRETALQKQVSLQVLEAQLQYRVLEAKHKTQLLRKQQTILDELQIOWK 256
QY 116 RRPETACIGGPNICLDRLNWTSLAESQLQTRQKIKLEELQKQVSYKGDPIVQHRPM 175
Db 257 RROQLAGNGPPGSLDVLQSWCEKLAETIWNQRQIRRAEHLCCQLPIPG-PVEEMLA 315
QY 176 LEEBIVELFRLNLMKSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLIV 224
Db 316 VNATITDIISALVTSTFIEIKQP-----PQVLKTQTKFAATVRLIV 356

RESULT 9
S5527
mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S5527; S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regula
A;Reference number: S5527; MUID:9518889; PMID:7862987
A;Accession: S5527
A;Molecule type: mRNA
A;Residues: 1-794 <WAK>
A;Cross-references: UNIPROT:P42231; EMBL:X78428; NID:9602354; PIDN:CAA55191.1; PID:g6023
A;Note: this is a revision to the sequence from reference S44353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 13, 2182-2191, 1994
A;Title: Mammary gland factor (MGF) is a novel member of the cytokine regulated transcri
A;Reference number: S44353; MUID:94244619; PMID:7514531
A;Accession: S44353
A;Molecule type: mRNA
A;Residues: 1-716, 'RHLHGSLPSR', 729, 'P', 731, 'ASL' <WAK>
A;Cross-references: EMBL:X78428
A;Note: this sequence has been revised in reference S5527
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 20.2%; Score 237; DB 2; Length 794;
Best Local Similarity 29.3%; Pred. No. 2.8e-08;
Matches 67; Conservative 41; Mismatches 99; Indels 22; Gaps 6;

QY 8 VTEKQMLEQLQDARKRVQDLQKMKVVENLQDDFDNY-KTLKSGQMDLNGN--- 63
Db 138 MSQKHLQINQTFEELRLVTDTELKQLOQTQYFIQYQESLRIOAQAQLAQLPQE 197
QY 64 ----QSVTRQKMQQLEQML-----TALDQMRSSIVSELAGLLSAMEYVQKTLTDEELADWK 115
Db 198 RLSRETALQKQVSLQVLEAQLQYRVLEAKHKTQLLRKQQTILDELQIOWK 257
QY 116 RRPETACIGGPNICLDRLNWTSLAESQLQTRQKIKLEELQKQVSYKGDPIVQHRPM 175
Db 258 RRDWRGWEAPPR-SLDVLQSWCEKLAETIWNQRQIRRAEHLCCQLPIPG-PVEEMLA 315

QY 176 LEEBIVELFRLNLMKSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLIV 224
Db 316 VNATITDIISALVTSTFIEIKQP-----PQVLKTQTKFAATVRLIV 356

RESULT 10
A54740
interleukin-4-induced transcription factor stat - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54740
R;Hou, J.; Schindler, U.; Hensel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
Science 265, 1701-1706, 1994
A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
A;Reference number: A54740; MUID:94367369; PMID:8085155
A;Accession: A54740
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-848 <HOU>
A;Cross-references: UNIPROT:P42226
C;Superfamily: human signal transducer and transcription activator STAT5A
C;Keywords: DNA binding; transcription regulation

Query Match 10.8%; Score 127; DB 2; Length 848;
Best Local Similarity 24.7%; Pred. No. 0.58;
Matches 59; Conservative 37; Mismatches 93; Indels 50; Gaps 9;

QY 3 PTAAVTEKQMLEQLQDARKRVQDLQKMKVVENLQDDFDNYKTLKSGQMDLNGN 62
Db 92 PLKLVAT-----FRQILQKKAV-----MEQFRHLPPFPHWKQBELFKTGLRLQHR 140
QY 63 NQSV--TROKMQQ-----LEQML-----TALDQMRSSIVSELAGLLSAMEYVQKTL 106
Db 141 VGEIHLRLALQKQVAGQVSLSLIETPANGTGPSEALMLIQTGLEA-----AKAL 196
QY 107 TDEELADWKRRPEIACIGGPNICLDRLNWTSLAESQLQTRQKIKLEELQKQVSYK 166
Db 197 VLKRIQIWKRRQQLAGNAP-----FEESLAPLQERCESLDIYSQLQVEGAAG 246
QY 167 DFI-VQHRPMLPEERIVELFRLNLMKSAFVVERQPCMPMPDRPLVKTGVQFTTKVRLIV 224
Db 247 GELEPKTRASLTGRDVLRLTIVTSCLFVEKQP-----PQVLKTQTKFQAGVRFLL 297

RESULT 11
I57557
DNA-Binding Protein and transcription factor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I57557
R;Quelle, F.W.; Shimoda, K.; Thierfelder, W.; Fischer, C.L.; Kim, A.; Ruben, S.M.; Clev
Mol. Cell. Biol. 15, 3336-3343, 1995
A;Title: Cloning of murine Stat6 and human Stat6, Stat proteins that are tyrosine phosph
A;Reference number: I57557; MUID:95280934; PMID:7760829
A;Accession: I57557
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-837 <RES>
A;Cross-references: UNIPROT:P52633; GB:L47650; NID:gl008876; PIDN:AAA79006.1; PID:gl008
C;Genetics:
A;Gene: STAT6
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 10.7%; Score 125.5; DB 2; Length 837;
Best Local Similarity 26.2%; Pred. No. 0.72;
Matches 61; Conservative 31; Mismatches 82; Indels 59; Gaps 10;

QY 10 EKQQMLEQ--HLQDARKRVQD-----LEQKMKVVENLQDDFDNYKTLKSGQMDQ 57
Db 106 EKKAVIEEPRHLPGPHRKQELKFTTTLGRLLHVRVRETRLLRESHLGPKT--GQVSLQ 163
QY 58 D-----LNGNOSVTRQKMQQLEQMLTALDQMRSSIVSELAGLLSAMEYVQKTLTDEELA 112

Db 164 NLIDPPNGPGPS-----EDLFTILO-----GVGDELTQ-PLVLLRIQ 202
QY 113 DMKRRPEIACIGPPNCLDRLENWITSLAESOLQTRQOIKKLE-BLQOKVSYKGDPIVQ 171
Db 203 IWKRQQLAGNGTFFPEESLAGLQRCESLVEIYSQLHQEIGAASGELEPKT-----253
QY 172 HRPMLERIVELFRNLKMSAFVVERQPCMPHDPRLVKTGVQFTTKVRLLV 224
Db 254 -RASLISRLDELVTLTVTSFLVEKQP-----PQVLKQTQKFGVRFLL 297

RESULT 12
AE1947
Chromosome segregation protein [imported] - Nostoc sp. (strain PCC 7120)
A:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE1947
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1947
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1208 <KUR>
A:Cross-references: UNIPROT:Q8YXT3; GB:BA000019; PIDN:BA073085.1; PID:g17130474; GSPDB:G17130474
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr1128
C:Superfamily: chromosome segregation protein SMC1

Query Match 10.5%; Score 122.5; DB 2; Length 1208;
Best Local Similarity 25.2%; Pred. No. 1.7;
Matches 58; Conservative 47; Mismatches 76; Indels 49; Gaps 11;

QY 5 AAVVTEKQKMLEQH--LQDARKVQDLE-QMKVVENLQDDFD--FNYKTLK-----S 52
Db 835 ATKTKTEQIQIRETAFRAEQRKLNLEQQOQLRERIQEAQQRITETQTTCTEAIN 894

QY 53 QGDMQDLNGNQ-SVTRQKMQLEQMLTALDQWRSIVSELQGLLSAMEYVQKLTDEEL 111
Db 895 RVSQQTNTTNAQITQTRAKLSELEQHLGAEKQKRDTEQEVSHLLRQOQLEWIKLEE 954

QY 112 ADWKRPEIACIGG-----PPNICLDRLNWNITSLAESOLQTRQOI---152
Db 955 TQLKRREDTALQSQLELVPNLPPEVDPKVDLEELQKELRSLAK-RLQAMEPVNML 1013

QY 153 -----KGLBELOQKV-SYKGDPIVQHRPMLERIVELFRNLKMSAF 192
Db 1014 ALLEYERTQKLELSQKLTLEGE-----RTELLARI-ENFTTLAQIAF 1057

RESULT 13
G72593
hypothetical protein APE1216 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: G72593
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kikuchi, Y. DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72593
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-533 <KAW>
A:Cross-references: UNIPROT:Q9YCP2; DDBJ:AF000061; NID:g5104821; PIDN:BA080205.1; PID:dl10382966
A:Experimental source: strain K1
C:Genetics:

A:Gene: APE1216

Query Match 10.4%; Score 122; DB 2; Length 533;
Best Local Similarity 21.2%; Pred. No. 0.73;
Matches 42; Conservative 48; Mismatches 66; Indels 42; Gaps 7;

QY 8 VTEKQMLEQHLQDARKRVQDLEQMKVVEN-----LQDDF-----DENYK 48
Db 319 MSQQLQALAELESLSRVEDLEARVGSVEDRLSQAEEEDISLTTSLSLRTBLEDLSTR 378
QY 49 TLKSCQDMQDLNGNQSVTRQKMQLEQMLTALDQWRSIVSELQGLLSAMEYVQKLTLD 108
Db 379 LAEAQASLEDLATRLDQVA-STLQQLQORLATAEESLQALTEDLASLQAEVTLQOSIVE 437
QY 109 BELADWKRPEIACIGPPNICLDRLNWNITSLAESOLQ-----TROQIKLEBLQOKVSY 164
Db 438 IDRLQLQRLSTVDV-----RLE--VESLGEKLVAEEKNQDASIEDFQSQIQ- 485
QY 165 KGDPIVQHRPMLERIVE 182
Db 486 -----ELRQLDEKTR 497

RESULT 14

A70387

conserved hypothetical protein aq_1006 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C:Accession: A70387

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; G

V. Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: A70387

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-978 <AQF>

A:Cross-references: UNIPROT:O67124; GB:AE000718; NID:g2983504; PIDN:AA07092.1; PID:g29

A:Experimental source: strain VF5

C:Genetics:

A:Gene: aq_1006

C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match

10.4%; Score 122; DB 2; Length 978;
Best Local Similarity 23.3%; Pred. No. 1.5;
Matches 49; Conservative 38; Mismatches 81; Indels 42; Gaps 6;

QY 10 EKQKMLEQHLQDARKRVQDLEQMKVVENLQDDFDNFYKTLKSGQDMQDLNGNQSVTRQ 69
Db 234 BEKDSLERELSQVVTKLLENLEKEVEKLEKLEFSRKVAP-----YVPIAK 281

QY 70 KMQQLEQMLTALDQWRSIVSELQGLLSAMEYVQKLT-----DEELAD- 113
Db 282 RIEEDDKLTTELKVRNKLTELAVLKDELSPAQEELNRIEAKFKFEKEREKELEHR 341

QY 114 WKRRPEIACIGPPNICLDRLNWNITSLAESOLQTRQOIKLEBLQOKVSYKGDPIVQHR 173
Db 342 LKKLQELKEI-----LKLSQLSSSLAKEKREYEQAKQEFEDLSERVE-KCKGLVAET 393

QY 174 PMLERIVELFRN-----LMKSAFVVERQ 197
Db 394 EEKLEKIKELFSEEEYTSLKMKERLILVELIQ 423

RESULT 15

T27075

hypothetical protein Y51A2D.16 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27075

R;McMurray, A.

submitted to the EMBL Data Library, January 1998

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2005, 17:15:30 ; Search time 95.284 Seconds
(without alignments)
1230.701 Million cell updates/sec

Title: US-10-090-185-31

Perfect score: 1172

Sequence: 1 NHPTAAVTEKQOMLEQHLQ.....IKTGQFTTKVRLLVKFPPEL 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1157	98.7	770	1 STA3 HUMAN	P40763 homo sapien
2	1157	98.7	770	1 STA3_MOUSE	P42227 mus musculus
3	1154	98.5	770	1 STA3_RAT	P52631 rattus norv
4	1150	98.1	770	1 STA3_BOVIN	P61635 bos taurus
5	1132	96.6	771	2 Q6DW79	Q6dv79 gallus gall
6	1099	93.8	769	2 Q9PVX8	Q9pvx8 xenopus lae
7	1096	93.5	766	2 Q7ZAK3	Q7zxx3 xenopus lae
8	1011	86.3	414	2 Q7ZTS5	Q7zts5 brachydanio
9	1011	86.3	765	2 Q6DVF3	Q6dvf3 oryzias lat
10	1011	86.3	785	2 Q6NV46	Q6nv46 brachydanio
11	1011	86.3	786	2 Q6GUE7	Q6gue7 oryzias lat
12	1011	86.3	806	2 Q93599	Q93599 brachydanio
13	987	84.2	764	2 Q90T16	Q90y16 tetraodon f
14	977	83.4	767	2 Q13133	Q13133 oncorhynch
15	656	56.0	163	2 Q9N145	Q9n145 macaca mula
16	575	49.1	751	2 Q8JGN0	Q8jgn0 xenopus lae
17	573	48.9	712	2 Q6P6Q7	Q6p6q7 rattus norv
18	573	48.9	749	2 Q9QXK0	Q9c497 mus musculus
19	571	48.7	749	2 Q8C497	Q99k94 mus musculus
20	570	48.6	712	2 Q99K94	Q8c3v4 mus musculus
21	570	48.6	749	2 Q8C3V4	Q9d323 mus musculus
22	570	48.6	749	2 Q9D323	Q8c8m3 mus musculus
23	570	48.6	755	2 Q8C8M3	P42224 homo sapien
24	569	48.5	750	1 STA1_HUMAN	Q68400 homo sapien
25	569	48.5	750	2 Q68D00	Q764m5 mus scrofa
26	569	48.5	757	2 Q764M5	P42225 mus musculus
27	562	48.0	749	1 STA1_MOUSE	Q13131 oncorhynch
28	540.5	46.1	754	2 Q13131	Q8jfu8 brachydanio
29	533	45.5	528	2 Q8JFU8	Q704w6 bos taurus
30	532.5	45.4	108	2 Q704W6	Q93598 brachydanio
31	532	45.4	749	2 Q93598	

32 532 45.4 749 2 Q6P943 Q6p943 brachydanio
33 531.5 45.3 718 2 Q801Y2 Q801y2 carassius a
34 520 44.4 748 1 STA4_HUMAN Q14765 homo sapien
35 519.5 44.3 758 2 Q90Y17 Q90y17 tetraodon f
36 517.5 44.2 754 2 Q13132 Q13132 oncorhynch
37 513 43.8 657 2 Q8AW24 Q8aw24 brachydanio
38 504.5 43.0 749 1 STA4_MOUSE F42228 mus musculus
39 504 43.0 651 2 Q7Z253 Q7z253 brachydanio
40 504 43.0 667 2 Q8AW20 Q8aw20 brachydanio
41 503.5 43.0 652 2 Q7Z277 Q7z277 brachydanio
42 503 42.9 553 2 Q8JFU7 Q8jfu7 brachydanio
43 503 42.9 748 2 Q6GHB2 Q6ghb2 rattus norv
44 503 42.9 1153 2 Q8JF55 Q8jfe5 brachydanio
45 491 41.9 737 2 Q90Y15 Q90y15 tetraodon f

ALIGNMENTS

RESULT 1
STA3_HUMAN
ID STA3_HUMAN STANDARD; PRT; 770 AA.
AC P40763; O14916; Q9BW54;
DT 01-FEB-1995 (Rel. 31, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
DE response factor).
GN Name=STAT3; Synonyms=APRF;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=94208062; PubMed=7512451; DOI=10.1016/S0378-1119(98)90235-6;
RA Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T.,
RA Yoshida K., Sudo T., Naruto M., Kishimoto T.,
RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
RT related transcription factor involved in the gp130-mediated signaling
RT pathway.";
RL Cell 77:63-71(1994).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98296260; PubMed=9630560; DOI=10.1016/S0378-1119(98)00185-1;
RA Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.,
RT "Highly conserved amino-acid sequence between murine STAT3 and a
RL revised human STAT3 sequence.";
RL Gene 213:119-124(1998).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM DEL-701), AND VARIANT ILE-143.
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattleSNPs, NHLBI HL6682 program for genomic applications, UW-
RL FHCRS, Seattle, WA URL: http://pga.gs.washington.edu.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND DEL-701).
RC TISSUE=Kidney, and Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RN SEQUENCE OF 564-704 FROM N.A.
RC TISSUE=Liver;
RC Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.,
RL Submitted (OCT-1997), to the EMBL/GenBank/DBJ databases.
RN [6]
RN PHOSPHORYLATION ON SERINE.
RX MEDLINE=95215843; PubMed=7701321;
RA Zhang X., Bienis J., Li H.-C., Schindler C., Chen-Kiang S.,
RA "Requirement of serine phosphorylation for formation of STAT-promoter
RT complexes.";
RL Science 267:1990-1994 (1995).
RN [7]
RN INTERACTION WITH NCOAL.
RX PubMed=11773079; DOI=10.1074/jbc.M111486200;
RA Giraud S., Bienvenu F., Avril S., Gascan H., Heery D.M., Coqueret O.,
RT "Functional interaction of STAT3 transcription factor with the
RT coactivator NcoA/SRC1a.";
RL J. Biol. Chem. 277:8004-8011 (2002).
CC -1- FUNCTION: Transcription factor that binds to the interleukin-6
CC (IL-6)-responsive elements identified in the promoters of various
CC acute-phase protein genes.
CC -1- SUBUNIT: Forms a homodimer or a heterodimer with a related family
CC member (at least STAT1). Interacts with NCOAL.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
CC in response to phosphorylation.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P40763-1; Sequence=Displayed;
CC Name=Del-701;
CC IsoId=P40763-2; Sequence=VSP_010474;
CC -1- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
CC muscle, kidney and pancreas.
CC -1- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
CC is important for the formation of stable DNA-binding STAT3
CC homodimers and maximal transcriptional activity.
CC -1- SIMILARITY: Belongs to the transcription factor STAT family.
CC -1- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC -----
CC EMBL; L29277; AAA58374.1; -;
CC EMBL; AJ012463; CAA10032.1; -;
CC EMBL; AY572796; AAS66986.1; -;
CC EMBL; BC000627; AAH00627.1; -;
CC EMBL; BC014482; AAH14482.1; -;
CC EMBL; AF029311; AAB84254.1; -;
CC PIR; A54444; A54444.
CC HSP; P42227; IBG1.
CC TRANSPAC; T01493; -;
CC Genew; HGNC:11364; STAT3.
CC H-InvdB; HIX0013840; -;
CC MIM; 102582; -;
CC GO; GO:0005737; Cytoplasm; TAS.
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0005062; F:hematopoietin/interferon-class (D200-domain. . .; TAS.

DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
DR GO; GO:0007122; P:negative regulation of transcription from P. . .; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2_
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT alpha; 1.
DR Pfam; PF02864; STAT bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
KW Activator; Alternative splicing; DNA-binding; Nuclear protein;
KW Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.
FT DOMAIN 580 670
FT MOD_RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD_RES 727 727 Phosphoserine (By similarity).
FT VARSPIC 701 701 Missing (in isoform Del-701).
FT VARIANT 32 32 /FTId=VSP_010474.
FT VARIANT 143 143 Q -> K (in dbSNP:1803125).
FT VARIANT 143 143 M -> I.
FT CONFLICT 288 288 /FTId=VAR_018679.
FT CONFLICT 460 460 Q -> H (in Ref. 1).
FT CONFLICT 548 548 P -> S (in Ref. 1).
FT CONFLICT 561 561 K -> N (in Ref. 1).
FT CONFLICT 667 667 F -> Y (in Ref. 1).
FT CONFLICT 730 730 V -> L (in Ref. 1).
FT CONFLICT 730 730 T -> A (in Ref. 1).
SQ SEQUENCE 770 AA; 88067 MW; 6C00632211C8012D CRC64;

Query Match 98.7%; Score 1157; DB 1; Length 770;
Best Local Similarity 98.7%; Pred. No. 2.9e-65;
Matches 226; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQMLBOHLQDARKVRQDLQKMKVVENLQDDFDNFYKTLKSGQMDQDLN 60
DB 130 NHPTAAVTEKQMLBOHLQDARKVRQDLQKMKVVENLQDDFDNFYKTLKSGQMDQDLN 189

QY 61 GNNQSVTRQKMQOQLTALDQMRRSIVSELAGLSAMEYVQKTLTDELDADWKRPEI 120
DB 190 GNNQSVTRQKMQOQLTALDQMRRSIVSELAGLSAMEYVQKTLTDELDADWKRQOI 249

QY 121 ACIGGPNICLDLENWITSLSAQLOTRQOIKLEELQKQVSKGDPVQHRPMLERI 180
DB 250 ACIGGPNICLDLENWITSLSAQLOTRQOIKLEELQKQVSKGDPVQHRPMLERI 309

QY 181 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKPEL 229
DB 310 VELFRNLKMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKPEL 358

RESULT 2
STAT3_MOUSE STANDARD; PRT; 770 AA.
ID STAT3_MOUSE
AC P42227;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Signal transducer and activator of transcription 3 (Acute-phase
DE response factor).
GN Name=Stat3; Synonyms=Aprf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185
RP AND 632-640.
RC STRAIN=BALB/c; TISSUE=Liver;
RC MEDLINE=94208062; PubMed=7512451; DOI=10.1016/0092-8674(94)90235-6;

RA Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,
 RA Yoshida K., Sudo T., Naruto M., Kishimoto T.;
 RA "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-
 RT related transcription factor involved in the gp130-mediated signaling
 RT pathway.";
 RL Cell 77:63-71 (1994).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RP
 RP TISSUE=Thymus;
 RX MEDLINE=94188718; PubMed=8140422;
 RA Zhong Z., Wen Z., Darnell J.E. Jr.;
 RA "Stat3: a STAT family member activated by tyrosine phosphorylation in
 RT response to epidermal growth factor and interleukin-6.";
 RL Science 264:95-98 (1994).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RP
 RP TISSUE=Brain;
 RX MEDLINE=95014185; PubMed=7523373;
 RA Raz R., Durbin J.E., Levy D.E.;
 RA "Acute phase response factor and additional members of the interferon-
 RT stimulated gene factor 3 family integrate diverse signals from
 RT cytokines, interferons, and growth factors.";
 RL J. Biol. Chem. 269:24391-24395 (1994).
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORM STAT3B).
 RP
 RP STRAIN=BALB/c, and C57BL/6; TISSUE=Liver;
 RX MEDLINE=96016116; PubMed=7568080;
 RA Schaefer T.S., Sanders L.K., Nathans D.;
 RA "Cooperative transcriptional activity of Jun and Stat3 beta, a short
 RT form of Stat3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101 (1995).
 RN [5]
 RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RP
 RP STRAIN=129/SvJ;
 RX PubMed=11161808; DOI=10.1006/geno.2000.6433;
 RA Miyoshi K., Cui Y., Riedlinger G., Lehoczy J., Zon L., Oka T.,
 RA Dewar K., Hennighausen L.;
 RA "Structure of the mouse stat 3/5 locus: evolution from Drosophila to
 RT zebrafish to mouse.";
 RL Genomics 71:150-155 (2001).
 RN [6]
 RN SEQUENCE FROM N.A. (ISOFORM STAT3A).
 RP
 RP STRAIN=C57BL/6J, and NOD/LtJ;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnanaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinska M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [8]
 RN PHOSPHORYLATION SITE SER-727, AND MUTAGENESIS.

RX MEDLINE=95354205; PubMed=7543024; DOI=10.1016/0092-8674(95)90311-9;
 RA Wen Z., Zhong Z., Darnell J.E. Jr.;
 RA "Maximal activation of transcription by Stat1 and Stat3 requires both
 RT tyrosine and serine phosphorylation.";
 RL Cell 82:241-250 (1995).
 RN [9]
 RN X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.
 RP MEDLINE=98334373; PubMed=9671298; DOI=10.1038/28101;
 RA Becker S., Groner B., Mueller C.W.;
 RA "Three-dimensional structure of the Stat3beta homodimer bound to
 RT DNA.";
 RL Nature 394:145-151 (1998)
 CC
 CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
 CC (IL-6)-responsive elements identified in the promoters of various
 CC acute-phase protein genes. STAT3B interacts with the N-terminal
 CC part of JUN to activate such promoters in a cooperative way.
 CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
 CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 CC member (at least STAT1). Interacts with NCOAL (by similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 CC in response to phosphorylation.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=Stat3A;
 CC IsoId=P42227-1; Sequence=Displayed;
 CC Name=Stat3B;
 CC IsoId=P42227-2; Sequence=VSP_006287;
 CC Name=Del-701;
 CC IsoId=P42227-3; Sequence=VSP_010475;
 CC -!- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and
 CC kidney. STAT3B is also detected in the liver, although in a much
 CC less abundant manner.
 CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 CC LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation
 CC is important for the formation of stable DNA-binding STAT3
 CC homodimers and maximal transcriptional activity (By similarity).
 CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
 CC -!- SIMILARITY: Contains 1 SH2 domain.
 CC
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 CC
 CC EMBL; L29278; AAA37254.1; -;
 CC EMBL; U06922; AAA19452.1; -;
 CC EMBL; U08378; AAA56668.1; -;
 CC EMBL; U30709; AAC52612.1; -;
 CC EMBL; AP246978; AAL59017.1; -;
 CC EMBL; AY299489; AAQ75418.1; -;
 CC EMBL; AY299490; AAQ75419.1; -;
 CC EMBL; BC003806; AAH03806.1; -;
 CC PIR; I49508; I49508.
 CC PDB; 1BG1; X-ray; A=1-722.
 CC TRANSFAC; T01574; -;
 CC MGD; MGI:103038; Stat3.
 CC GO; GO:0005737; Cytoplasm; IDA.
 CC GO; GO:0005634; C:nucleus; IDA.
 CC GO; GO:0005886; C:plasma membrane; IDA.
 CC GO; GO:0003677; F:DNA binding; IDA.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC GO; GO:0015563; F:transcriptional activator activity; IDA.
 CC GO; GO:0007259; P:JAK-STAT cascade; IDA.
 CC GO; GO:0006357; P:regulation of transcription from Pol II pro. .; IDA.
 CC InterPro; IPR008967; P53 like_DNA_bnd.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001217; STAT.
 CC Pfam; PF00017; SH2; 1.
 CC Pfam; PF01017; STAT_alpha; 1.
 CC Pfam; PF02864; STAT_bind; 1.


```
STA3_BOVIN          STANDARD;          PRT;   770 AA.
ID_STA3_BOVIN
AC_P61635;
DT_05-JUL-2004 (Rel. 44, Created)
DT_05-JUL-2004 (Rel. 44, Last sequence update)
DT_25-OCT-2004 (Rel. 45, Last annotation update)
DE_Signal transducer and activator of transcription 3.
GN_Name-STAT3;
OS_Bos taurus (Bovine).
OC_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC_Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC_Bovinae; Bos.
OX_NCBI_TaxID=9913;
RN [1]
RP_SEQUENCE FROM N.A.
RC_TISSUE=Mammary gland;
RA_Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
RT_The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus
during ruminant evolution."
RL_Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
(IL-6)-responsive elements identified in the promoters of various
acute-phase protein genes (By similarity).
CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.
CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
member (at least STAT1). Interacts with NCOA1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
in response to phosphorylation (By similarity).
CC -!- SIMILARITY: Belongs to the transcription factor STAT family.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ620655; CAF06182.1; -.
CC PROSITE; P55001; SH2; 1.
CC KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
KW Transcription regulation.
FT DOMAIN 580 670 SH2.
FT MOD RES 705 705 Phosphotyrosine (by JAK) (By similarity).
FT MOD RES 727 727 Phosphoserine (By similarity).
SQ_SEQUENCE 770 AA; 87974 MW; 9CEB147C73B83274 CRC64;

Query Match          98.1%; Score 1150; DB 1; Length 770;
Best Local Similarity 98.3%; Pred. No. 8.1e-65;
Matches 225; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 60
Db 130 NHPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLN 189
QY 61 GNNQSVTRQKMQQLEQMLTALDQMRISVSELAGLLSMEYVQKLTLDSELADWKRPEI 120
Db 190 GNNQSVTRQKMQQLEQMLTALDQMRISVSELAGLLSMEYVQKLTLDSELADWKRPEI 249
QY 121 ACIGGPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLERIV 180
Db 250 ACIGGPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLERIV 309
QY 181 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 229
Db 310 VELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 358

RESULT 5
Q6Dv79
ID Q6Dv79 PRELIMINARY; PRT; 771 AA.
AC Q6Dv79;
```

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DT_25-OCT-2004 (TrEMBLrel. 28, Created)
DT_25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT_25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE_Signal transducer and activator of transcription 3.
OS_Gallus gallus (Chicken).
OC_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC_Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC_Gallus.
OX_NCBI_TaxID=9031;
RN [1]
RP_SEQUENCE FROM N.A.
RC_Zhou G.Y., Leung F.C.;
RL_Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641397; AAT64887.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53_like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF001017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; P55001; SH2; 1.
SQ_SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;

Query Match          96.6%; Score 1132; DB 2; Length 771;
Best Local Similarity 96.9%; Pred. No. 1.1e-63;
Matches 221; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 HPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNG 61
Db 131 HPTAAVTEKQOMLEQHLQDARKRVQDLEQKMKVVENLQDDFDNFYKTLKSGQDMQDLNG 190
QY 62 NNQSVTRQKMQQLEQMLTALDQMRISVSELAGLLSMEYVQKLTLDSELADWKRPEIA 121
Db 191 NNQSVTRQKMQQLEQMLTALDQMRISVSELAGLLSMEYVQKLTLDSELADWKRPEIA 250
QY 122 CIGGPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLERIV 181
Db 251 CIGGPNICLDRLNWTSLAESQLQTRQOIKKLELOQKVS YKGDPIVQHRPMLERIV 310
QY 182 ELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 229
Db 311 ELFRNLMSAFVVERQPCMPMPDRPLVKTGQVFTTKVRLLVKPEL 358

RESULT 6
Q9PVX8 PRELIMINARY; PRT; 769 AA.
AC Q9PVX8;
DT_01-MAY-2000 (TrEMBLrel. 13, Created)
DT_01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT_01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE_Stat 3.
GN_Name=stat 3;
OC_Xenopus laevis (African clawed frog).
OC_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC_Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC_Xenopodinae; Xenopus.
OX_NCBI_TaxID=8355;
RN [1]
RP_SEQUENCE FROM N.A.
RX_MEDLINE=20107399; PubMed=10642787; DOI=10.1006/dbio.1999.9518;
RA_Nishinakamura R., Matsumoto Y., Matsuda T., Arizumi T., Heike T.,
RA_Asashima M., Yokota T.;
RT "Activation of Stat3 by cytokine receptor gp130 ventralizes Xenopus
embryos independent of BMP-4."
RT Dev. Biol. 216:481-490(1999).
DR EMBL; AB017701; BAA86061.1; -.
```


AC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OC NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY639947; AAT64912.1; -
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0004871; F:signal transducer activity; IEA.
DR GO: GO:0003700; P:transcription factor activity; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR DR InterPro; IPR008967; P53_like_DNA_bnd.
DR DR InterPro; IPR000980; SH2.
DR DR InterPro; IPR001217; SPAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
DR PROSITE; PS50001; SH2; 1.
DR SQ SEQUENCE 765 AA; 87566 MW; F5D01408748EC703 CRC64;
Query Match 86.3%; Score 1011; DB 2; Length 765;
Best local Similarity 84.8%; Pred. No. 5.2e-56;
Matches 195; Conservative 19; Mismatches 14; Indels 2; Gaps 2
QY 2 HPTAAVTEKQOMLEQHLQDARKEVDLEQKMKVVENLQDDFDNFYKTLKSGDM-QDLN 60
DB 130 HPTGTVTEKQQLLEHNLQDRIKRVQDMEQKMKMLELQDDFDNFYKTLKSGEUNQDLN 189
QY 61 GNNO-SVTRQKMQOLEQMLTALDOMRSIVSELAGLLSAMEYVQKLTLDDELADWKRRPE 119
DB 190 GNSQAATRQKMAQLEQMLSALDLRQRIVTEMGGLLTAMDYVQKNLTDELADWKRRQQ 249
QY 120 IACIGGPPNCLDRLENNITSLAESQLQTRQIKKLBELOKQSVYKGDPIVQHRPMLSEER 179
DB 250 IACIGGPPNCLDRLENNITSLAESQLQIRQIKKLBELOKQSVYKGDPIIQRPALSEK 309
QY 180 IVELFRNLMSAFVVERQCPMPHPDRPLVIKTGVQFTTKVRLVAKPPPEL 229
DB 310 IVDLFRNLMSAFVVERQCPMPHPDRPLVIKTGVQFTKNRLLLVAKPPPEL 359
RESULT 10
Q6GUE7 PRELIMINARY; PRT; 785 AA.
AC Q6GUE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Signal transducer and activator of transcription 3 isoform 1.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OC NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu R., Hong Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY641434; AAT46364.1; -
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0004871; F:signal transducer activity; IEA.
DR GO: GO:0003700; P:transcription factor activity; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR DR InterPro; IPR008967; P53_like_DNA_bnd.
DR DR InterPro; IPR000980; SH2.
DR DR InterPro; IPR001217; SPAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.

DR Pfam; PF02864; STAT bind; 1.
 DR Pfam; PF02865; STAT int; 1.
 DR PROSITE; PS50001; SH2; 1.
 SQ SEQUENCE 785 AA; 89643 MW; 81F231BDE27DE938 CRC64;

Query Match 86.3%; Score 1011; DB 2; Length 785;
 Best Local Similarity 84.8%; Pred. No. 5.3e-56;
 Matches 195; Conservative 19; Mismatches 14; Indels 2; Gaps 2;

QY 2 HPTAAVTEKQMLEQHLQDARKEVQDLQKMKVVENLQDDFDNFYKTLKSQDM-QDIN 60
 DB 130 HPTGTVVTEKQIIEHLNLDIRKRVQDMQKMKLENLQDDFDNFYKTLKSQELNQDIN 189
 QY 61 GNNQ-SVTRQKQKQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRPE 119
 DB 190 GNSQAATRQKMSQLEQLSALDQRRQIVTEMGELLTAMDYVQKLTDEELADWKRQ 249
 QY 120 IACIGGPPNICLDRLNWTSLAESQIQTRQIKKLEELQKQSVYKGDPIVQHRPMLER 179
 DB 250 IACIGGPPNICLDRLNWTSLAESQIQTRQIKKLEELQKQSVYKGDPIVQHRPALEEK 309
 QY 180 IVELFRNLMSAFVVERQPCMPHDPRLVIKTVQVQFTTKVRLLVKPEL 229
 DB 310 IVDLFRNLMSAFVVERQPCMPHDPRLVIKTVQVQFTTKVRLLVKPEL 359

RESULT 11
 Q6NV46 PRELIMINARY; PRT; 786 AA.

AC Q6NV46
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Stat3 protein.
 GN Name=stat3;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Deige J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC068320; AH68320.1; -;
 DR ZFIN; ZDB-GENE-980526-68; stat3.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR PROSITE; PS50001; SH2; 1.
 SQ SEQUENCE 786 AA; 90039 MW; FC7371D0B0E5447E CRC64;

Query Match 86.3%; Score 1011; DB 2; Length 786;
 Best Local Similarity 84.8%; Pred. No. 5.4e-56;
 Matches 195; Conservative 20; Mismatches 13; Indels 2; Gaps 2;

QY 2 HPTAAVTEKQMLEQHLQDARKEVQDLQKMKVVENLQDDFDNFYKTLKSQDM-QDIN 60
 DB 130 HPTGTVVTEKQIIEHLNLDIRKRVQDMQKMKLENLQDDFDNFYKTLKSQELNQDIN 189
 QY 61 GNNQ-SVTRQKQKQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKLTDEELADWKRPE 119
 DB 190 GNSQAATRQKMSQLEQLSALDQRRQIVTEMGELLTAMDYVQKLTDEELADWKRQ 249
 QY 120 IACIGGPPNICLDRLNWTSLAESQIQTRQIKKLEELQKQSVYKGDPIVQHRPMLER 179
 DB 250 IACIGGPPNICLDRLNWTSLAESQIQTRQIKKLEELQKQSVYKGDPIVQHRPALEEK 309
 QY 180 IVELFRNLMSAFVVERQPCMPHDPRLVIKTVQVQFTTKVRLLVKPEL 229
 DB 310 IVDLFRNLMSAFVVERQPCMPHDPRLVIKTVQVQFTTKVRLLVKPEL 359

RESULT 12
 O93599 PRELIMINARY; PRT; 806 AA.

AC O93599;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Transcription factor.
 GN Name=stat3;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 [1]
 RP SEQUENCE FROM N.A.
 RA Oates A.C.;
 RL Thesis (1998), University of Melbourne, Australia.
 DR EMBL; AJ005693; CAA06677.1; -;
 DR HSSP; P42227; 1BGI.
 DR ZFIN; ZDB-GENE-980526-68; stat3.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF01017; STAT alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS50001; SH2; 1.
 SQ SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;

Query Match 86.3%; Score 1011; DB 2; Length 806;
 Best Local Similarity 84.8%; Pred. No. 5.5e-56;

```
Matches 195; Conservative 20; Mismatches 13; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDLN 60
Db 130 HPTGTVTEKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDLN 189
QY 61 GNNQ-SVTRQKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDLN 119
Db 190 GNSQAARQKMAQLQDLRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 249
QY 120 IACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKQVYKGDPIVQHRPMLER 179
Db 250 IACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKQVYKGDPIVQHRPMLER 309
QY 180 IVELFRLNLMKSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPEL 229
Db 310 IVDLFRNLMKSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPEL 359

RESULT 13
Q90Y16 PRELIMINARY; PRT; 764 AA.
AC Q90Y16;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
SEQUENCE FROM N.A.
RA Sung S.C., Fan T.J., Leu J.H., Chou C.M., Huang C.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307106; AAL09415.1; -.
DR HSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF02864; STAT_alpha; 1.
DR Pfam; PF02865; STAT_int; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PS0001; SH2; 1.
SQ SEQUENCE 764 AA; 87411 MW; E661FFE18BEFD8BE CRC64;

Query Match 84.2%; Score 987; DB 2; Length 764;
Best Local Similarity 83.5%; Pred. No. 1.7e-54;
Matches 192; Conservative 20; Mismatches 16; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDLN 60
Db 130 NPSGTVTEKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDLN 189
QY 61 GNNQ-SVTRQKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDLN 119
Db 190 GNSQAARQKMAQLQDLRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 249
QY 120 IACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKQVYKGDPIVQHRPMLER 179
Db 250 IACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKQVYKGDPIVQHRPMLER 309
QY 180 IVELFRLNLMKSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPEL 229
Db 310 IVDLFRNLMKSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPEL 359

Matches 195; Conservative 20; Mismatches 13; Indels 2; Gaps 2;
QY 2 HPTAAVTEKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDLN 60
Db 130 HPTGTVTEKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDLN 189
QY 61 GNNQ-SVTRQKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDLN 119
Db 190 GNSQAARQKMAQLQDLRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 249
QY 120 IACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKQVYKGDPIVQHRPMLER 179
Db 250 IACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKQVYKGDPIVQHRPMLER 309
QY 180 IVELFRLNLMKSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPEL 229
Db 310 IVDLFRNLMKSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPEL 359
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RESULT 14
O13133 PRELIMINARY; PRT; 767 AA.
AC O13133;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE STAT3.
GN NamesrbtStat3;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8023;
RN [1]
SEQUENCE FROM N.A.
RA Johnson M.C., Mourich D.V., Leong J.C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U60333; AAB60926.1; -.
DR HSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001217; STAT.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
DR Pfam; PF02865; STAT_int; 1.
SQ SEQUENCE 767 AA; 87816 MW; FED97740C74C3798 CRC64;

Query Match 83.4%; Score 977; DB 2; Length 767;
Best Local Similarity 81.4%; Pred. No. 7.4e-54;
Matches 188; Conservative 24; Mismatches 17; Indels 2; Gaps 2;
QY 1 NHPTAAVTEKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDL 59
Db 129 SHPSGTVTEKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDL 188
QY 60 GNNQ-SVTRQKQMLEHQLDARKRVQDLQKMKVVENLQDDFDNFYKTLKSQGM-QDL 118
Db 189 NGNSQAARQKMAQLQDLRRQIVTEMAGLLSAMDVFQKNTLDEELADWKRRQ 248
QY 119 ETACIGPPNICLDRLENWITSLSAQSLOTRQIKKLEELQKQVYKGDPIVQHRPMLER 178
Db 249 QIACIGGPPKICLDRLETWITSLSGRIQLQIRQIKKLEELQKQVYKGDPIVQHRPMLER 308
QY 179 RIVELFRLNLMKSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPEL 229
Db 309 KIVDLFRNLMKSAFVVERQPCMPHDPRLPVIKTGVOFTTKVRLLVKFPPEL 359

RESULT 15
O9N145 PRELIMINARY; PRT; 163 AA.
AC O9N145;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Signal transducer and activator of transcription (Fragment).
GN Name=STAT3;
OS Macaca mulatta (rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
SEQUENCE FROM N.A.
RA Arredondo J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
```

DR EMBL; AF227560; AAF73401.1; -.
DR HSSP; P42227; 1BG1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008967; P53 like_DNA_bnd.
DR InterPro; IPR01217; STAT.
DR Pfam; PF01017; STAT_alpha; 1.
DR Pfam; PF02864; STAT_bind; 1.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 18855 MW; DD3F11E7F5B9878C CRC64;

Query Match 56.0%; Score 656; DB 2; Length 163;
Best Local Similarity 98.4%; Pred.No.3.le-34;
Matches 126; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 102 VQKTLTDEELADWKRRPEIACIGGPPNICLDRLNWTSLAESOLQTRQIKKLEELQOK 161
Db 1 VQKTLTDEELADWKRRQIACIGGPPNICLDRLNWTSLAESOLQTRQIKKLEELQOK 60

Qy 162 VSYKGDPIVQHRPMLERIVELFRNLKSAFVVERQPCMPHDPDRPLVINTGVQFTTKVR 221
Db 61 VSYKGDPIVQHRPMLERIVELFRNLKSAFVVERQPCMPHDPDRPLVINTGVQFTTKVR 120

Qy 222 LLVKFPPEL 229
Db 121 LLVKFPPEL 128

Search completed: May 25, 2005, 17:43:45
Job time : 96.284 secs